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OM protein - protein search, using sw model

July 16, 2001, 16:35:41; Search time 56.06 Seconds (without alignments) 12.977 Million cell updates/sec Run on:

US-09-786-648-3 62 Title: Perfect score: Sequence:

1 VEVPGSQHIDSQ 12

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

412676 segs, 60623988 residues Searched: 412676 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

/SIDSB/gcgdata/geneseq/geneseqp/AA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score		Query Match Length DB ID	DB	ID	Description
	62	100.0	12	21	AAY87461	Cholera toxin B/en
7	62	100.0	15	10	AAP93498	CTP3 epitope of th
m	62	100.0	15	16	AAR85125	Cholera toxin B an
4	62	100.0	21	21	AAY87462	Cholera toxin B/en
5	62	100.0	21	21	AAY87463	E. coli heat labil
9	62	100.0	23	16	AAR76748	Residues 50-64 of
7	62	100.0	56	4	AAP30265	Sequence of amino
80	62	100.0	41	9	AAP50439	Network polymer wh
6	62	100.0	46	9	AAP50436	Network polymer wh
10	62	100.0	47	4	4 AAP30600	Sequence of amino
11	62	100.0	93	16	AAR72545	ADP-ribosylating t

Escherichia coli v	E. coli heat-labil	Heat labile toxin	E coli verotoxin-1	Sequence of sub-un	Synthetic cholera	Heat labile entero	Cholera toxin B su	Cholera toxin B su	Amino acid sequenc	Cholera Toxin B-su	B subunit of the h	Cholera toxin B su	Amino acid sequenc	Plant-optimized E.	Plant-optimized V.	GtfB.1/CTB chimeri	LIB-CIB fusion pro		Sequence of LT-B-M	Recombinant exotox	Recombinant exotox	Recombinant exotox	LTB-CTP fusion pro	Labile toxin (LT-B	C. jejuni flagelli	HSV-1 antigen/heat	B subunit of CT.	Adhesin/V.cholerae		Helicobacter pylor	Adhesin/CTXA2B chi	Cholera toxin B su	
AAY41816	AAW95226	AAY68365	AAB66239	AAP50340	AAW04857	AAR94939	AAW06606	AAW06607	AAW80808	AAR04163	AAP93561	AAW06605	AAW59770	AAY96652	AAY96872	AAR12630	AAR04825	AAB73241	AAR50227	AAB73242	AAB73243	AAB73244	AAW94082	AAY01300	AAW67443	AAR11272	AAR28831	AAW74466	AAW80599	AAW80600	AAY32094	AAB15525	SCOOLURE
20	20	21	22	9	17	17	17	17	19	11	10	17	19	21	21	12	11	22	15	22	22	22	20	20	20	12	13	19	19	19	20	21	ć
93	93	93	93	103	103	103	103	103	103	118	124	124	124	124	124	126	131	134	138	142	155	163	170	371	371	405	124	461	749	1338	461	15	4
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	90.3	90.3	0	90.3	79.0	75.8	97
62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	. 29	62	62	62	62	62	62	62	62	62	62	62	26	26	99	26	49	47	
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32		34	35	36	37	38	39	40	4.1	42	43	44	u .

ALIGNMENTS

RESULT AAY87461

AAY87461 standard; peptide; 12 AA.

AAY87461;

03-JUL-2000 (first entry)

Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:3.

EtxB; Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.

Vibrio cholerae. Escherichia coli.

WO200014114-A1.

16-MAR-2000

99WO-GB02970. 07-SEP-1999; 98GB-0019484. 07-SEP-1998;

(UYBR-) UNIV BRISTOL.

Williams NA, Hirst TR;

WPI; 2000-256943/22.

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor GM-1

0; Gaps

Indels

Score 62; DB 10; Pred. No. 4.1e-05; Mismatches 0;

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100.0%;

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12

Length 15;

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oligonucleotides to form a new recombinant gene. This encodes a flagellin fusion protein which can be used in vaccines for immuno-
subunit. The DNA sequence encoding this ligates to othersynthetic
                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                1 VEVPGSQHIDSQ 12
                                                                     Seguence
                                          therapy
                                                                                                                                                                                                                                                     AAR85125
                                                                                                                                                                                                                                       RESULT
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                                 The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera to toxin (Ctx) from vibrio cholerae which do not bind to the ubiquitous from vibrio collerae which do not bind to the ubiquitous composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (App) Appribosyltransferase activity, while the B subunits (EtxB and CtxB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible or some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the cornal EtxB and CtxB, except that they do not bind or cross link GM-1. They may also be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. They may also be used as an inhibitor for toxin-induced diarrhoea. They may also be used as an inhibitor for toxin-induced diarrhoea. Composition for composition for treathny, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 chartholanly wreferred peptides of the invention, AAY87460 being
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New recombinant flagellin gene including sequence – for heterologous epitope, and expressed fusion proteins, useful in vaccines and for prodn.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTP3 epitope of Cholera toxin B subunit; flagellin fusion protein; vaccine; immunotherapy; ds;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PRAX-) PRAXIS BIOLOGICS INC.
(STRD ) LEYLAND STANDFORD JUNIOR UNIV.
             Disclosure; Page 15; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP93498 standard; protein; 15 AA.
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AAP93498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccines for oral immunisation against infecting agents, e.g. cholera - comprise a conjugate of an antigen of an infecting agent covalently bound to micro:particulate inert carrier, e.g. modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A compsn. comprising a conjugate of an antigenic cholera B toxin peptide fragment (e.g. AAR8126-30 and esp. AAR81212), covalently bound to a microparticulate inert carrier (e.g. modified silica or thyroglobulin) can be used as an oral vaccine for immunisation against cholera infection. The inert carrier is insoluble in the digestive tract, allowing presentation of the antigen in the intestines, where it will elicit antibodies mainly of the
                                                                                                                                                                                                                        Conjugate; cholera: B toxin; peptide fragment; microparticulate; inert carrier; modified silica; thyroglobulin; oral vaccine; immunisation; infection; insoluble; digestive tract; antigen; intestines; secretory; IgA class.
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100.0%; Pred. No. 4.1e-05;
tive 0; Mismatches 0;
                                                                                                                                                                      Cholera toxin B antigenic peptide fragment CTP3.
AAR85125 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 25; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sela M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (YEDA ) YEDA RES & DEV CO LTD.
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                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                       Vibrio cholerae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAY-1994;
                                                                                                               13-JUN-1996
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                                                       AAR85125;
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This sequence corresponds to the CTP3 epitope of the Cholera toxin B

Disclosure; fig.4B; 137pp; English.

1 vevpgsqhidsq 12

qq

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The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from vibrio cholerae which do not bind to the ubiquitous (M-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (AbP) Abpribosyltransferase activity, while the B subunits (EtxB and CtxB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the cormal EtxB and Ctx, it has been found that certain effects of the toxins, such as immunomodulation are fragments of the cormal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may also be used an medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAV87460-Y87463 represent preferred peptides of the invention, AAY87460 being
                                                                                                                                                                                     Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Derivatives of Escherichia coli heat labile enterotoxins useful a immunomodulators and for treating diarrhea and which do not bind glycolipid receptor {\tt GM-1} .
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                                                                                                                                              Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 15; 62pp; English.
                   AAY87462 standard; peptide; 21 AA.
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                   Vibrio cholerae.
Escherichia coli.
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                                                            AAY87462;
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AAY87462
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Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor GM-1

98GB-0019484.

07-SEP-1998; 07-SEP-1999; 16-MAR-2000

(UYBR-) UNIV BRISTOL.

WPI; 2000-256943/22.

Williams NA,

Disclosure; Page 15; 62pp; English.

Heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.

Escherichia coli. WO200014114-A1.

E. coli heat labile enterotoxin B-derived peptide, SEQ ID NO:5.

(first entry)

03-JUL-2000

AAY87463;

AAY87463 standard; peptide; 21 AA.

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The invention relates to peptide fragments of the Escherichia coli heat corn labile enterotoxin (Etx) and its closely related homologue, cholera (CC labile enterotoxin (Etx) and its closely related homologue, cholera (CC labile enterotoxin (Etx) end closely related homologue, choleras (CX) its responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-crosponsible for toxicity, possessing adenosine diphosphate (ADP) ADP-crosponsible for toxicity, while the B subunits (EtxB and CtxB) cribosyltransferase activity, while the B subunits (EtxB and CtxB) cross-linking of GM-1 receptors. Although GW-1 binding is responsible cross-linking of GM-1 receptors. Although GW-1 binding is responsible cross-linking of GM-1 receptors. Although GW-1 binding is responsible crosponsible crosponsible crosponsible crosponsible crosponsible crosponsible crosponsible crosponsible crosponsible data and Ctx it has been found that certain effects of EtxB and/or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link crosmal EtxB and CtxB subunits, except that they do not bind or cross link crosponsible crospo
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100.0%; Pred. No. 5.9e-05;
Live 0; Mismatches 0;
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RESULT AAR76748

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Gaps

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1 VEVPGSQHIDSQ 12

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5 vevpgsqhidsq 16

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AAR76748 standard; Protein; 23 AA

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AAP30265 standard; Protein; 26 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is encoded by a fragment of the the plasmid ptPpA93
which was used in the production of fimH fusion genes comprising
the cholera toxin B subunit inserted into the fimH gene. This insert
shows the inclusion of the B subunit into the FimH protein at position
214-226. The chimmeric genes were then opt. further modified by insertion
of the hepatitis B virus surface antigen pre-S2 region into a different
of the hepatitis B virus surface antigen pre-S2 region into a different
cof the hepatitis B virus surface antigen pre-S2 region into a different
position of the FimH adhesin of type I fimbriae. Restiction site handles
(BglII-sites) were introduced into the fimH gene, and the foreign
epitopes are then inserted in-frame. In the selected positions the
insertion of the FimH protein. The expression of the chimmeric proteins
on the surface of fimbriae on bacterial hosts illustrated the possibility
of using bacterial adhesins as general presenters of foreign antigens and
epitopes. These chimmeric genes may be used in the production of variant
FimH adhesins which may be useful for targetting active compounds
con an intendial cells to locations comprising selected receptors to which
                                                                                                   FimH; type 1 fimbriae; organelle; adhesin; alpha-D-mannoside residue; FimA; FimF; FimG; receptor binding site; PCR; amplify; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor specific bacterial adhesins - useful for targetting active compounds and microbial cells to locations of receptors
                                                                          Residues 50-64 of cholera toxin B subunit and FimH 224-226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sokurenko EV;
                                                                                                                                                                                                                                            5..19
/note= "Cholera toxin B subunit 50-64"
                                                                                                                                                                                                      'note= "Represents FimH residue 224"
                                                                                                                                                                                                                                                                                                         /note= "Represents FimH residue 226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pallesen L,
                                                                                                                                                                                                                       "..4
'note= "Linker peptide"
                                                                                                                                                                                                                                                                   20..22
/note= "Linker peptide"
                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; Page 58; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molin S,
                                                                                                                                        Chimeric - Vibrio cholerae.
Chimeric - Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                  95WO-DK00042.
                                                                                                                                                                                                                                                                                                                                                                                                          94US-0187166.
                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   (GXBI-) GX BIOSYSTEMS AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hasty DL, Klemm P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-275442/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and microbial celthe adhesins bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ93061
                                                                                                                                                                              Key
Misc-difference
                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-1994;
                                                                                                                                                                                                                                                                                                                                 WO9520657-A1
                                                                                                                                                                                                                                                                                                                                                                                 27-JAN-1995;
                                                18-MAR-1996
                                                                                                                                                                                                                                                                                                                                                         03-AUG-1995
                         AAR76748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                    Peptide
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The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30660). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coli (enterotoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as a vaccine 1-10mg of active cpd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Network polymer which comprises a series of composite E. coli heat-labile toxin (LT)/heat-stable toxin (ST) polypeptide repeating untis.
                                            Sequence of amino acids 50-75 of the cholera toxin Bl subunit which carries an Arg at posns. 67 and 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                     Cholera vaccine; therapy; E.coli infection; enterotoxin LT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dodin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 62; DB 4; Length 26
100.0%; Pred. No. 7.4e-05;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rivaille P, Siffert O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP50439 standard; protein; 41 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CNRS ) CNRS CENT NAT RECH SCI. (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 11; 13pp; French
                                                                                                                                                                                                                                                                                                                                                                                                       82FR-0009167.
                                                                                                                                                                                                                                                                                                                                                     83EP-0401052.
21-APR-1992 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Milhaud G, Raulais D, F
Guyongruaz A, Delmas A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 VEVPGSQHIDSQ 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 AA;
                                                                                                                                                                                            Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                     26-MAY-1983;
                                                                                                                                                                                                                                                                                                                                                                                                       26-MAY-1982;
                                                                                                                                                                                                                                                                                                   30-NOV-1983.
                                                                                                                                                                                                                                            EP95426-A.
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1 VEVPGSQHIDSQ 12

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Gaps

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Indels

Length 23;

Query Match 100.0%; Score 62; DB 16; Best Local Similarity 100.0%; Pred. No. 6.5e-05; Matches 12; Conservative 0; Mismatches 0;

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The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coli (enterotoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as a vaccine 1-10mg of active cpd.
                                                                                                               interpolypeptide cystine bonds formed between oxidized cys residues of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. The composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala or Glu, X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP50439-57.
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of amino acids 350-75 of the cholera toxin B1 subunit which carries an Arg at posns. 35, 67 and 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
                                                                                                                                                                                                                                                                                                                                               ö
New synthetic polypeptide(s) for part of E. coli enterotoxin(s useful for vaccination of mammals against the enterotoxin(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera vaccine; therapy; E.coli infection; enterotoxin LT
                                                                                                                                                                                                                                                                                                       100.0%; Score 62; DB 6; Length 46; 100.0%; Pred. No. 0.00014; ive 0; Mismatches 0; Indels
                                                                                           The repeating units are bonded together by intramolecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dodin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Siffert 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rivaille P,
                                                      Claim 8; Page 100; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAP30600 standard; Protein; 47 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Page 11; 13pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CENT NAT RECH SCI
PASTEUR.
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                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 10v.v.
Ass 12; Conservative
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Guyongruaz A, Delmas A;
                                                                                                                                                                                                                                                                                                                                                                                    12
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                                                                                                                                                                                                                                                                                                                                                                                                          16 vevpgsqhidsq
                                                                                                                                                                                                                                                                                                                                                                                      1 VEVPGSQHIDSQ
                                                                                                                                                                                                                                                  46 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-APR-1992
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                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The repeating units are bonded together by intramolecular interpolypeptide cystine bonds formed between oxidized cys residues of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. The composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala or Glu, X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP50439-57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Network polymer which comprises a series of composite E. coli heat-labile toxin (LT)/heat-stable toxin (ST) polypeptide repeating untis.
                                                                                                                                                                                                                                                                                                                                                              New synthetic polypeptide(s) for part of E. coli enterotoxin(s useful for vaccination of mammals against the enterotoxin(s)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 62; DB 6; Length 41; Best Local Similarity 100.0%; Pred. No. 0.00012; Matches 12; Conservative 0; Mismatches 0; Indels
              Heat-labile enterotoxin; heat-stable toxin; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heat-labile enterotoxin; heat-stable toxin; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                      8; Page 100; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP50436 standard; protein; 46 AA.
                                                                                                                                                                     84WO-US02030
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                                                                                                                                                                                                                                              (SCRI-) SCRIPPS CLINIC RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1985-159230/26.
                                                                                                                                                                                                                                                                                                                         WPI; 1985-159230/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 AA;
                                                                                                                                                                     12-DEC-1984;
                                                                                                                                                                                                          12-DEC-1983;
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                                                                                                                                                                                                                                                                                     Houghten RA;
                                                                                         WO8502611-A
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                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
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ADP-ribosylating toxin; PT; crystalline pertussis holotoxin; ETA; DT; three-dimensional structure; LT; immunoprotective; infection.
                                                                                                                                                                                                                                                                                                                                                New method for producing modified pertussis holotoxin
                                                                          Escherichia coli verotoxin-1 B-subunit.
AAY41816
ID AAY41816 standard; peptide; 93 AA.
                                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 5; 41pp; English.
                                                                                                                                                                                                                                                             (CONN-) CONNAUGHT LAB LTD. (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                              Stein PE,
Oomen RP;
                                                                                                                                                                                                                                                                                                                            WPI; 1999-579908/49.
                                                                                               ADP-ribosylating
                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                  22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
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                                                     08-DEC-1999
                                                                                                                                                    US5965385-A
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                                AAY41816;
                                                                                                                                                                                                                                                                                              Read RJ,
                                                                                                                                                                                                                                                                                                        Hazes B,
             ô
                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR72540-R72545 are structurally equivalent B-subunits from three ADP-ribosylating toxins, pertussis holotoxtin (PT), E. coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify sites which contribute to PT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New modified forms of pertussis holotoxin - developed using crystalline forms of pertussis holotoxin and its complexes with
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Loosmore S;
                                Length 47;
                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 62; DB 16; Length 9
Best Local Similarity 100.0%; Pred. No. 0.0003;
Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                      ADP-ribosylating toxin; pertussis holotoxin; B-subunit; active site; E. coli heat labile toxin; verotoxin-1; Bordetella pertussis vaccines.
                              100.0%; Score 62; DB 4; I
100.0%; Pred. No. 0.00014;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hazes B, Klein MH,
                                                                                                                                                                                                                  ADP-ribosylating toxin (verotoxin-1 B-subunit).
                                                     Mismatches
                                                                                                                                                AAR72545 standard; peptide; 93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 5; 54pp; English.
                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Armstrong GD, Cockle SA, Ha
Oomen R, Read RJ, Stein PE;
                                                                                                                                                                                                                                                                                                                                                                     93US-0110947.
94US-0251121.
                                                                                                                                                                                                                                                                                                                                                 94EP-0306219
                                                                                                                                                                                                                                                                                                                                                                                                     (CONN-) CONNAUGHT LAB LTD. (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                              (first entry)
                                                     Conservative
                                                                        1 VEVPGSQHIDSQ 12
                                                                                      WPI; 1995-132623/18.
                              Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pertussis infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other molecules
 47
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                                                                                                                                                                                                                                                                                                                                                                     24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                              28-NOV-1995
                                                                                                                                                                                                                                                                                 Bacteria sp.
                                                                                                                                                                                                                                                                                                                            05-APR-1995,
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                                                                                                                                                                       AAR72545;
 Sequence
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Armstrong GD;

Klein MH,

Loosmore S,

Cockle SA,

94US-0292968. 93US-0110947. 94US-0251121.

95US-0467974.

(first entry)

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Involving analysis of the 3-dimensional form of the crystalline involving analysis of the 3-dimensional form of the crystalline holotoxin. The pertursis holotoxin modification process comprises:

(1) identification of at least one amino acid (as) residue of the holotoxin for modification by analysing the 3-dimensional form of the crystalline holotoxin, in relation to known information of the protein structure and function; (2) effecting mutagenesis (by removing or replacing a nucleotide sequence encoding at least one (as)) of a tox operon; and (3) expressing mutant tox box in a Bordetella organism to produce the modified holotoxin. This method is used for modifying pertussis holotoxin, by studying its 3-dimensional crystalline structure. Modifying the holotoxin, alters its blological properties. By analysing the 3-dimensional crystalline structure of the pertussis holotoxin can be identified. This can be used to predict (as) which contribute to the toxicity of the holotoxin to produce immunoprotective, genetically-detoxified analogues of pertussis holotoxin. The present sequence represents an ADP-ribosylating toxin to be accounted by the pertussis holotoxin. The present sequence represents an ADP-ribosylating toxin the present in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW95226 standard; peptide; 93 AA.
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Conservative C
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Best Local Similarity
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Matches
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AAW95226
ID AAW9
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Gaps

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1 VEVPGSQHIDSQ 12 Vevpgsghidsg 51

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40

12

RESULT

Length 93;

us-09-786-648-3.rag

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Heat labile toxin B subunit SEQ ID NO:26
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Oomen RP;
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                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 - AUG - 1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAY-1994;
                                                                                                                                                   immunogenic.
                                                                                                                                                                                                                                                             US6018022-A.
                                                                                                                                                                                                                                                                                                                     25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Read RJ,
Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB66239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to methods of preparing a pertussis holotoxin (PT) having a modified biological activity. One method comprises identifying at least 1 site in a PT that interacts with a molecule that is capable of forming a complex with the holotoxin and which molecule is an effector molecule which is an adenine nucleotide and which site contributes to toxicity, cell binding or enzymatic activity of PT. The functional interacting site(s) are identified by analysing the three dimensional structure of crystalline PT, determined by X-ray crystallogaphy. The identified interacting site(s) are modified to alter toxicity, cell binding or enzyme activity of the PT. The methods can be used to alter a biological activity such as toxicity, enzymatic activity, mitogenicity, cell binding and adjuvanticity of the PT. The three-dimensional structure of crystallogaphy or structural resemblance to other bacterial toxins such as diphtheria toxin (DT), Pseudomonas exotoxin A (ETA), the heat-labile toxin of E. coli (LT) and verotoxin-1 (VT). The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modifications to e.g. enzymatic activity, mitogenicity and cell binding of pertussin holotoxin - by identifying interaction sites of a molecule with crystalline toxin and modifying the identified site
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                                                                                                                                                               Pertussis holotoxin; PT; modified; effector; toxicity; cell binding; enzyme; ADP-ribosylation; toxin; crystalline; X-ray crystallography; structural analysis; interacting site; mitogenicity; adjuvanticity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loosmore
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                                                                                                             E. coli heat-labile toxin (LT) beta-subunit sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klein MH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3D, Cockle SA, Hazes B,
Read RJ, Stein PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 5; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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ilarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-0292968.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94US-0292968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0110947
94US-0251121
                                                          (first entry)
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                       heat-labile; LT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-1994;
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                                                        16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-AUG-1993;
31-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                            05-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                       US5856122-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Armstrong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
AAW95226;
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The present invention describes a crystalline form of isolated pertussis holotoxin, in which the molecules of pertussis toxin have a three dimensional structure represented in the specification.

The complexed with a polyaaccharide molecule capable of forming a complex with the holotoxin. The crystalline form of the pertussis holotoxin can be used in a comparison with other proteins which have functional resemblance to pertussis holotoxin with the aim of modifying other proteins. Identifying the unknown sites of toxicity by comparison with the three dimensional structure of pertussis holotoxin provides a technique for detoxification of toxins to produce useful immunogenic but non-toxic analogues. It can also be used as a primary standard to measure the quantity, purity or efficacy of less pure compositions containing pertussis toxin. AAY68340 to AAY68385 represent peptides used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein MH, Armstrong GD;
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Pertussis toxin; heat labile toxin; verotoxin, exotoxin A; holotoxin diphtheria toxin; ADP-ribosylating toxin; mannose binding protein; infection; crystal structure; X-ray crystallography; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crystalline form of isolated pertussis holotoxin useful in studying proteins which have functional resemblance -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 0.0003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cockle SA, Loosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E coli verotoxin-1 B subunit SEQ ID NO: 26.
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100.0%; Pr
tive 0;
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94US-0251121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CONN-) CONNAUGHT LAB LTD.
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Best Local Similarity 100.

Matches 12; Conservative
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Escherichia coli.

US6168928-B1

02-JAN-2001

Oomen RP,

Cockle SA,

Stein PE;

Read RJ, Hazes B,

WPI; 2001-122260/13.

(CONN-) CONNAUGHT LAB LTD.

94US-0292968. 93US-0110947. 94US-0251121. 98US-0082514.

24-AUG-1993; 31-MAY-1994;

21-MAY-1998; 22-AUG-1994; Example 3; Fig 5; 41pp; English.

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The inventors claim vaccines against cholera and heat-labile E.coli toxin contg. cholera toxin fragment coupled to carrier. The toxin is esp. the fragments defined in FT, above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant constructs for expressing and opt. secreting proteins in Bordetella - comprise Bordetella promoter coupled to non-Bordetella, esp. cholera B toxin, gene or coupled to non-Bordetella leader and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cholera toxin B subunit; enzyme; antigen; immunogen; allergen; enzyme inhibitor; hormone; lymphokine; immunoglobulin; toxin; structural protein; receptor; heterologous gene; leader; promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant constructs comprising a promoter functional in Bordetella operatively linked to a heterologous gene or a non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella pertussis; whooping cough; recombinant construct;
                                                                                                                                                                                                                                                                                                                                                                                            Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                   Vaccines against cholera and heat-labile E. coli toxin cholera toxin fragment coupled to carrier
                                                                                                                                                                                                                                                                                                                                                                                          Score 62; DB 6; I
Pred. No. 0.00034;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Loosmore SM, Yacoob RK, Zealey GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW04857 standard; Protein; 103 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic cholera toxin B subunit.
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                                                                                                                                                                                                                                                                                                                                                                                            100.0%; ; ; 100.0%; 1
                                                                                 (YEDA ) YEDA RES & DEV CO LID.
                                                                                                                                                                                                                                       Example; Fig 1; 24pp; German.
                                               83IL-0069558.
              84DE-3430894.
                                                                                                                  Sela M, Arnon R, Jacob CO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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N-PSDB; AAT38038.
                                                                                                                                                    WPI; 1985-069683/12
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                             103 AA;
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            22-AUG-1984;
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                                               23-AUG-1983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein MH,
                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention provides a method for producing a pertussis toxin (also designated lymphocytosis promoting factor, histamine-sensitising factor and islet activating protein) with a modified biological activity, involving analysing the crystal structure of the protein to identify active sites which can then be modified. This may lead to an alteration in the toxicity, cell binding or enzyme activity of the toxin. This can be used in the production of immunoprotective analogues of pertussis toxin is the cause of whooping cough following infection by Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                       Modifying pertussis holotoxin to produce detoxified PT analogs, comprising analyzing crystalline structure of toxin, to identify sites of toxicity, cell binding or enzyme activity of PT and modifying identified site
                                                                                                                                                                                                                                       Klein MH, Armstrong GD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 62; DB 22;
100.0%; Pred. No. 0.0003;
Live 0; Mismatches 0;
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Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative

93 AA;

Sequence

1 VEVPGSQHIDSQ 12

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40 vevpgsqhidsq

RESULT 16 AAP50340 8..20 /note= "claimed" 45..64 /note= "claimed"

DE3430894-A. 14-MAR-1985.

50..64 /note= "claimed"

Region Region Region

Vibrio cholera

(first entry)

01-DEC-1991

AAP50340;

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Gaps

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Bordetella leader sequence for secretion of a gene product which may not be of Bordetella origin, can be used for the expression in Bordetella of enzymes, antigens, immunogens, allergens, enzyme inhibitors, hormones, immunoglobulins or their fragments, toxins, mammalian proteins, structural proteins or treceptors. The Bordetella strains are particularly engineered to express the cholera toxin B subunit (this sequence). The promoters used in the constructs are selected from the Bordetella pertussis tox, that promoters or the high molecular weight (hmw) outer membrane promoter of non typable Haemophilus influenzae; leaders used in the pertussis toxin subunit S1 leader (S1-L) and the pertussin pertactin leader (PRN-L); and genes used in the constructs are selected from the choice toxin B leader (CTB-L), the constructs are selected from the choice of synthetic cholera toxin B gene (ctb) and the hmw1 and hmw2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A transgenic plant comprising or expressing a DNA sequence encoding an immunogenic agent can be used as an oral vaccine for animals. The vaccine is administered by the oral consumption of the plant and provides the first known functional method for immunising animals using transgenic plants, where the plants express bacterial antigens that act as both immunogens and adjuvants. The method provides an inexpensive production and edlivery system for such antigens to animals. This is the LT-B Escherichia coli toxin subunit and its coding sequence was used in the construction of such a transgenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 62; DB 17; Length 103; 100.0%; Pred. No. 0:00034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR94939 standard; Protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes of Haemophilus influenzae
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N-PSDB; AAT18799, AAT18800.
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les 12; Conserv
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Matches
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Gaps
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plant. The immunogenic agent preferably comprises the LT-B or CT-B (cholera toxin B subunit) or optionally LT-A or CT-A.
                                                                                                                                                                                                                                                                                                                    Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid.
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                                                                                Length 103;
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replaced by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         replaced by Asn'
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/note= "wild-type Ala replaced by
                                                                                100.0%; Score 62; DB 17; 100.0%; Pred. No. 0.00034;
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Chimeric - Enterotoxigenic Escherichia Coli
                                                                                                           0; Mismatches
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/note= "wild-type Thr
Misc-difference 94
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/note= "wild-type His
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                                                                                Query Match 100.

Best Local Similarity 100.
Matches 12; Conservative
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LEBENS M R.
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                                                                                                                                      1 VEVPGSQHIDSQ
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                                         103
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Gaps

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Length 103; 0; Indels

Score 62; DB 17; Pred. No. 0.00034; 0; Mismatches

100.0%; 100.0%;

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immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic lliness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.

Note - This sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                   1 VEVPGSQHIDSQ 12
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                                                                                                                                   AAW06605)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW06607 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to
protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.

Note - This sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid.
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/label- substitution
/label- first 25 amino acids of mature
/note- wild-frye cholera toxin B subunit are
wild-type cholera toxin B subunit are
replaced with the first 25 amino acids
of mature enterotoxin B subunit"
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                                                                                                                                                                                   100.0%; Score 62; DB 17; Length 103; 100.0%; Pred, No. 0.00034;
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Chimeric - Enterotoxigenic Escherichia Coli.
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                                                                                                                                                                Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vomiting; food poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Holmgren J, Lebens MR;
                                                                                                                                                                                                                                               1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-506108/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R.
                                                                                                                                   103 AA;
                                                                                                                                                                                                                                                                     Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT43577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9634893-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-1996
                                                                                                     AAW06605).
                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 AAW06607;
     888888888
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This is the amino acid sequence of the cholera toxin B subunit used in the method of the invention involving the use of nontoxic subunits as an effective adjuvant in coadministration of an antigen to birds and animals. In addition to the use of the toxin as an mucosal adjuvant, it also provides a vaccine comprising the toxin, an immunogenic amount of an antigen, and a pharmaceutically acceptable carrier. The toxin can be used with single/multiple vaccines, and it humans, since these are more effective and safer than vaccines administered subcutaneously.
                                                                                                                           Cholera toxin B subunit, nontoxic subunit; adjuvant, coadministration; antigen; bird, animal; mucosal; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New mutant cholera toxin selected from a group comprising nontoxic subunits/derivatives - effective as an adjuvant when coadministered with an antigen to birds and mammals
                                                                                             Amino acid sequence of the wild type chorela toxin B subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                            Takeda Y, Yamamoto
AAW80808 standard; protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 1B; 43pp; English.
                                                                                                                                                                                                                                                                     98WO-US06725.
                                                                                                                                                                                                                                                                                                  97US-0043410
                                                                29-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                              (KIYO/) KIYONO H.
(MCGH/) MCGHEE J R.
(TAKE/) TAKEDA Y.
(UABR-) UAB RES FOUND.
(YAMA/) :YAMAMOTO S.
                                                                                                                                                                                                                                                                                                                                                                                                                             Kiyono H, Mcghee JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-594478/50.
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103 AA;

Seguence

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subunit of the heat-labile enterotoxin (LT-B) derived from E. coli.
                                                                                                       B subunit; heat-labile enterotoxin; LT-B; Escherichia coli; malari, circumsporozoite protein; fusion protein; live recombinant vaccine; Salmonella; epitope.
                                                                                                                                                                                                                                          1..22
/note="Signal peptide"
23..124
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                          /note="Mature LT-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pillai S,
                                                                                                                                                                                                                                                                                                                                                                                                       88WO-US03376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PRAX-) PRAXIS BIOLOGICS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                           87US-0104735
                                    06-JUN-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Majarian WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1989-114399/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAN90747.
                                                                                                                                                                                 Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                       30-SEP-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-1997
                                                                                                                                                                                                                                                                                                                              WO8902924-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  multivalent
                                                                                                                                                                                                                                                                                                                                                                   06-APR-1989
AAP93561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW06605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brey RN,
                                                                                                                                                                                                                       Key
Peptide
                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    In the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 24
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   NAMES OF THE PROPERTY OF THE P
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                                                                                                                                                                                                                                                                                                                                                                                    cholera toxin B-subunit; hybrid protein; heterologous IgA active antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mature cholera toxin B-subunit is obtained when the signal peptide is cleaved off. There is an Ochre codon at position 343-5; the sequence downstream from it is part of a plasmid.
                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New hybrid protein, useful in vaccines \mbox{\,{}^{\text{-}}} contains cholera toxin b subunit and heterologous IgA active
                                    Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 118;
                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..11
/*label= signal peptide
/*note= absent from mature protein
                                    DB 19;
0.00034;
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100.0%; Score 62; DB 11;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 12; Conservative 0; Mismatches 0;
                                100.0%; Score 62; DB
100.0%; Pred. No. 0.0
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYLI-) L'UNIVERSITE DE L'ETAT A LIEGE.
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/*label- His or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP93561 standard; protein; 124 AA.
                                                                                                                                                                                                                                   AAR04163 standard; protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Martial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88FR-0012627
                                                                                                                                                                                                                                                                                                           (first entry)
                                  Ouery Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; ; pp; French.
                                                                                                                                                                                                                                                                                                                                               Cholera Toxin B-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Renard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fillillillilli
61 vevpgsqhidsq 72
                                                                                                          1 VEVPGSQHIDSQ 12
                                                                                                                                           50 vevpgsqhidsq 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1990-132273/17
N-NSDB; Q04046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antigenic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-SEP-1988;
                                                                                                                                                                                                                                                                                                           10-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                    synthetic
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                                                                                                                                                                                                                                                                         AAR04163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region
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AAP93561
ID AAP9
                                                                                                                                                                                                                     AAR04163
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Hockmeyer WT;

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protein with an epitope of a malaria parasite, eg Region I or Region II or a repeat region of circumsporozoite protein antigen (CS) (AAP93560) from Plasmodium berghei. Pref. the fusion gene is inserted into attenuated Salmonella enteriditis under the left promoter control of lambda. Such bacteria can multiply in the host without causing disease or disorder and express CS that will induce a protective immune response against malaria and can be used in vaccines. Such vaccines can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cholera toxin B subunit, used for hybrid immunogenic toxin production.
                                                                                                                                                                                                                     patent, the DNA encoding LT-B is expressed as part of a fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; CTB; heat labile enterotoxin B subunit; LTB; vaccine; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 124;
                             comprising attenuated entero-invasive bacterium contg. DNA encoding epitope of malaria parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
0.00041;
thes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 62; 100.0%; Pred. No.
Live recombinant vaccine for malaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW06605 standard; Protein; 124 AA
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                                                                                                                                          Fig 3; p. 3/17; 105pp; English.
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96US-0747410

Ireland J;

97WO-US20584

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(UNMS ) UNIV MICHIGAN STATE.
                                                                                                                                         WPI; 1998-297947/26.
                                                                                                                                                    N-PSDB; AAV41573;
                                                                                                                   Bagdasarian M,
          WO9821344-A1
                                                    12-NOV-1997;
                                                                          L2-NOV-1996;
                                22-MAY-1998
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                                                                                                                                                                                                                                                                                                                                                      AAW06605 is the full (including the signal peptide) length cholera toxin B subunit (CTB), this sequence is described as unpublished in the specification. The mature CTB protein was used to create hybrid mutants, in which certain amino acids (aa) of CTB were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB), see AAW06605 and AAW06607. The specific amino acids substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                          Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
immunogen; antigen; broad spectrum; cross reactive; diarrhoea; vomiting; food poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 62; DB 17; Length 124; 100.0%; Pred. No. 0.00041;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                 1..21
/label= sig_peptide
                                                                                    22..124
/label- mat_protein
                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW59770 standard; Protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 32pp; English
                                                                                                                                                              96WO-SE00570
                                                                                                                                                                                    95SE-0001682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                       Holmgren J, Lebens MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                         WPI; 1996-506108/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 AA
                                                                                                                                                                                                                                                                      N-PSDB; AAT43575
                              Vibrio cholerae,
                                                                                                                                                                                  05-MAY-1995;
                                                                                                                                                              02-MAY-1996;
                                                                                                                   WO9634893-A1
                                                                                                                                         07-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW59770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                               Peptide
                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 2
                                                       Key
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Beta-subunit of heat labile enterotoxin; LTB; fusion protein; vaccine; immunogen; antigen; inhibin; fertility; follicle stimulating hormone;

FSH; sperm; ova; immune response.

Escherichia coli.

Amino acid sequence of E. coli LTB.

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                                                                                                                                                                                                                                     This is the amino acid sequence of Escherichia coli beta-subunit of heat labile enteritoxin (LTB). It is used in the method of the invention to create fusion proteins which are useful as vaccinating immunogens. The fusion proteins are useful in vaccines, specifically where the antigenic peptide is an inhibin fragment for increasing the fertility of an animal (by increasing levels of follicle stimulating hormone (FSH) or production of sperm or ova), but more generally for inducing an immune response against the antigenic peptide. Vaccines are particularly administered orally, e.g. fusion protein is expressed in edible plants or animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
New nucleic acid encoding fusion of antigenic peptide and enterotoxin sub-unit - useful as vaccinating immunogen, particularly for increasing animal fertility by inducing antibodies against inhibin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 62; DB 19;
llarity 100.0%; Pred. No. 0.00041;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: July 16, 2001, 16:35:41 Job time: 205 sec
                                                                                                                                                                                    Disclosure; Fig 9; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 AA;
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LENGTH: 93 amino acids
IYPE: amino acid
              3860
3860
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3860
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STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino ac
STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                          US-08-292-968-26
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Sequence 2, Appli
Patent No. 5194375
Sequence 1, Appli
Sequence 4, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21, Appl
                                                                                                                  (without alignments)
7.978 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Al Sequence 26, Al Sequence 2, Ap Sequence 2, Ap Sequence 2, Ap Sequence 21, Ap Sequence 21, A Sequence 2, Ap Sequence 3, Ap Sequence 2, Ap Sequence 3, Ap Sequence 2, Ap Sequence 3, Ap Sequence 4, Ap Sequence 5, Ap Sequence 6, Ap Seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 34,
Sequence 2, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                July 16, 2001, 16:36:18; Search time 30.3 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-09-082-514-26
US-08-952-337-5
US-08-952-337-6
US-08-472-171-2
US-08-013-047-2
US-09-1013-047-2
US-09-1013-047-2
US-09-101-852-21
PCT-US59-13376-21
US-08-952-337-1
US-08-952-337-2
US-08-952-337-2
US-08-829-026A-6
US-08-435-65A-12
US-08-435-65A-12
                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-602-359A-34
US-08-878-989-2
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-08-467-976-26
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US-09-039-609-4
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US-09-027-337-2
                                                                                                                                                                                                                                                                                      193259 seqs, 20144635 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                           Listing first 45 summaries
                                                                 OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                              US-09-786-648-3
62
1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match Length
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                                                                                                                                                                 Title:
Perfect score:
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                                                                                                                                                                                                     Sequence:
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US-09-039-609-2
US-08-416-950-11
US-07-672-304-3
US-07-672-304-3
US-08-611-398B-4
US-08-64-4051-4
US-08-64-4051-4
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US-08-674-612-3
US-08-674-612-3
US-08-674-612-3
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US-08-950-448A-14
US-08-950-448A-14
US-08-950-448A-14
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US-08-950-968-904-2
US-09-286-904-46
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APPLICANT: STEIN, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COOMEN, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARASTRONG, Glen D.
APPLICANT: ARASTRONG, Glen D.
APPLICANT: MORES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENE ADDRESS:
ADDRESSEE: Sim & MCBULDEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REALBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,968
                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1038-388
Sequence 26, Application US/08292968 Patent No. 5856122 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEO ID NO: 26:
SEQUENCE CHARACTERISTICS:
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OPERATING SISTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
PALICATION NUMBER:
FILING DATE:
CLASSIFICATION:
APPLICATION:
435
PRIOR APPLICATION:
APPLICATION NUMBER:
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APPLICATION NUMBER:
CLASSIFICATION NUMBER:
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APPLICATION NUMBER:
APPLICATION NUMBER:
BRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER:
APPLICATION NUMBER:
APPLICATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MODIFICATION OF PERTUSSIS TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 62; DB 2; 100.0%; Pred. No. 0.00027; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Toronto
STATE: Ontario
COUTRY: Canada
ZIP: MAG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATINE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                             Sequence 26, Application US/08467536 Patent No. 5977304
                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COCKLE, Stephen A.
APPLICANT: LOCSWORE, Sheena
APPLICANT: LOCSWORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
ITLE OF INVENTION: WODIFICATION
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARATERISTICS:
LENGTH: 93 amino acids
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Best Local Similarity 100.
Matches 12; Conservative
                                   1 VEVPGSQHIDSQ 12
                                                                       40 VEVPGSQHIDSQ 51
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                                                                                                                                                                                            RESULT 3
US-08-467-536-26
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US-08-467-976-26
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                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: STEIN, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COOMEN, Raymond P.
APPLICANT: LOOSWORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,974
                                                                                           Score 62; DB 2; I Pred. No. 0.00027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: STEWART Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-454 MIS:vg
                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION 1435

PRIOR APPLICATION DATE: US 08/467,536

FILING DATE: 06-UN-1995

APPLICATION NUMBER: US 08/292,968

FILING DATE: 22-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121

FILING DATE: 31-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947

FILING DATE: 24-AUG-1993

ATTORNEY AGENT INFORMATION:
WANTER AND ATTORNEY AGENT AND ATTORNEY AGENT ATTORNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Application US/08467974
Patent No. 5965385
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                                                                                           100.0%;
100.0%;
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26
                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                   1 VEVPGSQHIDSQ 12
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Best Local Similarity
Matches 12; Conserva
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US-08-467-974-26
US-08-292-968-26
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Gaps

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Length 93; Indels

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Sequence 5, Application US/08952337

Sequence 5, Application US/08952337

Patent No. 6019973

GENERAL INFORMATION:
APPLICANT: Holmaren, Jan
TITLE OF INVENTION: HYBRID MOLECULES BETWEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEN HEAT-LABILE
CURRENT APPLICATION HYBRID MOLECULES BETWEEN B SUBUNITS
FILE REFERENCE: 3846/000758

CURRENT APPLICATION NUMBER: US/08/952,337

CURRENT FILING DATE: 1996-01-05

EARLIER APPLICATION NUMBER: PCT/SE96/00570

EARLIER PILING DATE: 1996-05-02

EARLIER PILING DATE: 1995-05-05

NUMBER OF SEQ ID NOS: 6

SOFTWARE PRESENCE FOR WINDOWS Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 62; DB 4; Length 93; 100.0%; Pred. No. 0.00027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                        ALDERSEE: SING & MCBUINEY
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTR: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Datentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/082,514
FILLING DATE:
                                                TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                           ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: STERRARI MICHAEJ I.
REGISTRATION NUMBER: 24,973
REPERENCE/DOCKET NUMBER: 1038-810
TELEPHONE: (416) 595-1155
     ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT; ORGANISM: Vibrio cholerae
US-08-952-337-5
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US-08-952-337-5
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                                                                  APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: STEIN, Stephen A.
APPLICANT: COCKLE, Stephen A.
APPLICANT: LOOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
CORRESPONDENCE SIM & MCBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/467,976
FILING DATE: 06-UNN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/09082514
Patent No. 6168928
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: OOKELE, Stephen A.
APPLICANT: OOMEN, RAYMOND P.
Sequence 26, Application US/08467976
Patent No. 6018022
                                                                                                                                                                                                                                                                                                                                                                   STREET: Suite 701, 330 Univer:
CITY: Toronto
STATE: Ontario
COUNTR: Canada
ZIP: MSG 187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOSFWARE: PatentIn Release #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               READ, Randy J.
STEIN, Penelope E.
COCKLE, Stephen A.
OOMEN, Raymond P.
KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VEVPGSQHIDSQ 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-082-514-26
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APPLICANT: LOSMOTOR, Sheena M
APPLICANT: LOSMOTOR, Reza K
APPLICANT: Yacoob, Reza K
APPLICANT: Yacoob, Reza K
APPLICANT: Yacoob, Gavin R
APPLICANT: Klein, Michel H
TITLE OF INVENTION: EXPRESSION OF GENE PRODUCTS FROM
TITLE OF INVENTION: GENETICALLY MANIPULATED STRAINS OF BORDETELLA
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS: SIM & MCBURNEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
STREET:
STREET:
CITY: Toronto
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,526
FTLING DATE: 01-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62; DB 2;
Pred. No. 0.0003;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62; DB 2;
Pred. No. 0.0003;
                                                        NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 1038-507 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-59-1153
TELEPA: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Sequence 2, Application US/08894526

Patent No. 5942418

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET UNMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
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Best Local Similarity 100.0%;
Matches 12; Conservative 0
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                             : 103 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 103 amino acids
amino acid
                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-472-171-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                          LENGTH:
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APPLICANT: Loosmore, Sheena M.
APPLICANT: Loosmore, Sheena M.
APPLICANT: Zealey, Gavin R.
APPLICANT: Zealey, Gavin R.
APPLICANT: Zealey, Gavin R.
APPLICANT: Sealey, Gavin R.
APPLICANT: Sealey, Gavin R.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains of Bordetella
TITLE OF INVENTION: Genetically Manipulated Strains of Bordetella
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: September 5.56
CORRESPONDENCE ADDRESS:
ADDRESSES: 330 University Avenue, Suite 701
STREET: 330 University Avenue, Suite 701
STREET: And Condation
COUNTRY: Canada
ZIP: M5G IR?
COMPUTER: Canada
ZIP: M5G IR?
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                    Gaps
                                                                  ;
0
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APPLICANT: Holmgren, Jan

APPLICANT: Holmgren, Jan

APPLICANT: LOBENS, MICHAEL R.

TITLE OF INVENTION: HUTBRID MOLECULES BETWEEEN HEAT-LABILE

TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS

TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS

TITLE OF INVENTION: BY SECOND SECOND SECOND SERVICE TOXIN B SUBUNITS

CURRENT APPLICATION NUMBER: DC/08/952,337

CURRENT FILING DATE: 1996-01-05

EARLIER PILING DATE: 1996-05-05

EARLIER FILING DATE: 1996-05-05

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NOS: 6
              Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 102;
100.0%; Score 62; DB 3; Length Lu
100.0%; Pred, No. 0.0003;
""" """ "" " Indels
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APPLICATION NUMBER: US/08/472,171 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,334
                                                                                                                                                                                                                                                                        Sequence 6, Application US/08952337 Patent No. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08472171 Patent No. 5932714
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0
                 100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT; ORGANISM: Escherichia coli
US-08-952-337-6
            Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                      49 VEVPGSQHIDSQ 60
                                                                                                           1 VEVPGSQHIDSQ 12
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US-08-952-337-6
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TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
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Patent No. 6194560
GENERAL INFORMATION:
APPLICANT: Charles J. Arntzen, Hugh S. Mason, and Tariq A. Hag
TILLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER, READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/374,597
                                                                                                   NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 1301 McKinney, Suite 5100 CITX: Houston STATE: TX
                                                                                                                                                                                                            STATE: Ontario
COUNTRY: Canada
ZIP. MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1038-964
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/393,334
FILING DATE: FEBRUARY 23, 1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
TELEFAX: 065-24567 simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
APPLICANT: Yacoob, Reza K. APPLICANT: Zealey, Gavin R. APPLICANT: Klein, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 103 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein US-09-374-597-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VEVPGSQHIDSQ 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: US
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                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: Accob, Reza K.
APPLICANT: Accob, Reza K.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains of Bordetella
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MoBurney
STREET: 330 University Avenue, 6th Floor
CITY: TOTORIO
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
  Gaps
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  Indels
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APPLICATION NUMBER: US/09/013,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 62; DB 2; L
100.0%; Pred. No. 0.0003;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR PAPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,171
FILING DATE: 07-4UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,334
FILING DATE: 23-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFENDE/DOCKET NUMBER: 1038-507 MIS:V9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: M5G 1N,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-POS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09374597
Patent No. 6140082
GENERAL INFORMATION:
APPLICANT: LOSEMORE, Sheena M.
                                                                                                                                                                    US-09-013-047-2
; Sequence 2, Application US/09013047
; Patent No. 5998168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQUENCE CHARACTERISTICS:
; LENGTH: 103 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-013-047-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 416-595-1163
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
Conservative
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                                                               50 VEVPGSQHIDSQ 61
12;
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Matches
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Gaps

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100.0%; Score 62; DB 5; Length 103; 100.0%; Pred. No. 0.0003; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                     Sequence 1, Application US/08952337 Patent No. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT; ORGANISM: Eschcerichia col1
US-08-952-337-2
                                                            Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT; ORGANISM: Vibrio cholerae US-08-952-337-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Conservative
                                                                                                                           1 VEVPGSQHIDSQ 12
                                                                                                                                                    1 VEVPGSQHIDSQ 12
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Best Local Similarity
Matches 12; Conserv
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US-08-952-337-1
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                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: The Texas A&M University System
APPLICANT: 310 Wisenbaker
APPLICANT: 310 Wisenbaker
APPLICANT: 310 Wisenbaker
TITLE ON INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 62; DB 4; Length 103; llarity 100.0%; Pred. No. 0.0003; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Houston
STATE: TX
COUNTRY: 100
COUNTRY: 100
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
FILING DATE: 24-OCT-1995
APPLICATION NUMBER: 08/817,906
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/328,716
FILING DATE: 24-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: JONES, JOHN W.
REGISTRATION NUMBER: 31,380
REFERENCE/DOCKET NUMBER: 36170/3P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                P01590US1
APPLICATION NUMBER: US/09/191,852 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US95-13376-21; Sequence 21, Application PC/TUS9513376; GENERAL INFORMATION:
                                                                                                                                                                                NAME: FOX, DATIG I.

REGISTRATION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: P0155
TELECOMMUNICATION INFORMATION:
TELEPAX: 713-651-5151
TELEPAX: 713-651-5151
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
TOPOLOGY: linear
US-09-191-852-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 VEVPGSQHIDSQ 61
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Matches 12; Conserv
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Sequence 2, Application US/08952337

Batent No. 6019973

GENERAL INFORMATION:

APPLICANT: Holmayen, Jan

APPLICANT: Holmayen, Jan

APPLICANT: Holmayen, Jan

APPLICANT: Holmayen, Jan

TITLE OF INVENTION: BYTEROTOXIN AND CHOLERA TOXIN B SUBUNITS

FILE REFERENCE: 3846/00758

CURRENT APPLICATION NUMBER: US/08/952,337

CURRENT APPLICATION NUMBER: PCT/SE96/00570

EARLIER APPLICATION NUMBER: PCT/SE96/00570

EARLIER FILING DATE: 1996-05-02

BARLIER FILING DATE: 1996-05-05

SOFTWARE: FALSKO DATE: 1995-05-05

SOFTWARE: PSSESQ for Windows Version 3.0

SECTION 2.
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                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Holmgren, Jan
APPLICANT: Holmgren, Jan
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REPERENCE: 3846/0D758
CURRENT APPLICATION NUMBER: 105/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER PILING DATE: 1999-05-02
EARLIER PILING DATE: 1999-05-05
EARLIER PILING DATE: 1995-05-05
EARLIER FILING DATE: 1995-05-05
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 123
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ilarity 100.0%; Pred. No. 0.00037;
Conservative 0; Mismatches 0;
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Matches 12; Conserva
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US-08-449-045C-4
Sequence 4, Application US/08449045C
Patent No. 5770203
GENERAL INFORMATION:
APPLICANT: Burnette, Neal W.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Inc.
                                                                                                                                                            COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN ROLAS:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/829,026A
FILING DATE: 18-AUG-1997
CLASSIFICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REGISTRATION NUMBER: 35,024
RELEPHONE: 301-504-5676
TELEFRAM: 301-504-5676
TELEFRAM: 301-504-5676
SEQUENCE CHARACTERISTICS:
TENECOMMUTO FOR SED ID NO: 6:
SEQUENCE CHARACTERISTICS:
TENECHMENTION ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,045C
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Janelle S. Graeter
STREET: Room 411, Building 005, BARC-W
CITY: Beltsville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UMBER: US/08/449,045C
24-MAY-1995
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CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/694,733
FILING DATE: 02-MAY-1991
PRIOR APPLICATION DATE: US 08/271,222
APPLICATION NUMBER: US 08/271,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 371 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California
COUNTRY: USA
ZIP: 91320-1789
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                                                                                                                                         COUNTRY:
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APPLICANT: Meinersmann, Richard J.
APPLICANT: Khoury, Christian A.
TITLE OF INVENTION: Campylobacter Jejuni Flagellin-Escherichia Coli LT-B Fusion P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                        Sequence 2, Application US/08747410

Patent No. 5993820

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BAGDASARIAN, Michael
APPLICANT: IRELAND, James
TITLE OF INVENTION: CHIMERIC LTB VACCINES
TOWNERS OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 5993820west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: DASACTE
COMPUTER: IBM COMPAIABLE
COMPUTER: DOS
COMPUTER: DOS
COMPUTER: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ESSIGN DOS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,410
FILING DATE: 12-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION BATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 33,924
RECISTRATION NUMBER: 33,924
REFERENCE/COCKET NUMBER: 11526.1-US-01
TELECHONNUM. 112/311-5268
TELECHONEN: 612/311-5268
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US-08 829-026A-6
'Sequence 6, Application US/08829026A
'Patent No. 5837825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Some Best Local Similarity 100.0%; P. Matches 12; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VEVPGSQHIDSQ 12
                                                 70 VEVPGSQHIDSQ 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: ORIGINAL SOURCE: US-08-747-410-2
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US-08-747-410-2
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                                       PAPELICANT: Burton, Frank H.:Sutcliffe, Gregor

TITLE OF INVENTION: CHOLERA TOXIN GENE REGULATED BY GROWTH

TITLE OF INVENTION: CHOLERA TOXIN GENE REGULATED BY GROWTH

HORMONE PROMOTER

NUMBER OF SEQUENCES: 18

CURRENT APPLICATION DATA:

FILING DATE: 18-MAY-1990
                                                                                                                                                                                                                                                                             Score 56; DB 6; Length 124;
Pred. No. 0.0044;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: FISH & RICHARDSON P.C. STREET: 4225 EXECUTIVE SQUARE, STE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09010/010001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
ODERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,355
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-602-359A-34; Sequence 34, Application US/08602359A; Patent No. 5942430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: February 16, 1996
CLASSIECATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MORENTSON, Daniel E.
MURPHY, Dennis
REID, John
MAFFIA, Anthony
LINK, Steven
SWANSON, Ronald V.
WARREN, Patrick V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: HAILE, LISA 3.
RECISTRATION NUMBER: 38.347
REFERENCE/DOCKET NUMBER: 0901
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPHONE: 619-678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KOSMOTKA, Anna
TITLE OF INVENTION: ESTERASES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 34:
                                                                                                                                                                                                                                                                                 90.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 346 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                 Query Match 90.3
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: LINEAR MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: LA JOLLA
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                         1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                    , LENGTH: 124
5223610-3
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-435-605A-12
Sequence 12, Application US/08435605A
FRETCH NO. 58742B
FRETCH NO. 58742B
FRETCH NO. 58742B
FRETCHT: Kaalow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
FUNDERS OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATE: US/08/435,605A
FILING DATE: 05-MAY-1995
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                                                                                                                                                                                                                                                                               Query Match 90.3%; Score 56; DB 1; Length 124; Best Local Similarity 91.7%; Pred. No. 0.0044; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.3%; Score 56; DB 2; Length 124; 91.7%; Pred. No. 0.0044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
NAME: Mazza, Richard J.
REGISCRATION UNDBER: 27,657
REFERENCE/DOCKET NUMBER: A-19
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 mino acids
TYPE: anino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                           ; MOLECULE TYPE: protein US-08-449-045C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-435-605A-12
                                                                                                                                                                                                                                                                                                                                                         1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                            1 VEVPGSQHIDSQ 12
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US-08-602-359A-34

20

RESULT

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Sequence 2, Application US/09027337B
Sequence 2, Application US/09027337B
Patent No. 5972616
GENERAL INFORMATION:
APPLICANT: UNFORMATION:
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TANG-15: An Extracellular Serine Protease Overexpressed in TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 448;
                                                         GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Corley, Nail C.
APPLICANT: Guegler, Karl G.
APPLICANT: Guegler, Karl G.
APPLICANT: Guejler, Karl G.
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
ITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CNERBYN APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 4
Pred. No. 44;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                        Sequence 2, Application US/09272796 Patent No. 6207148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 59.7
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LIBRARY: TBLYNOT01
CLONE: 40194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                              Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                  USA
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US-09-027-337-2
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    Score 39; DB 2; Length 346;
Pred. No. 15;
4; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Shah, Purvi
TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
TITLE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 2;
Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERNCE/DOCKET NUMBER: PF-0321 US
TELECOMNUNICATION INFORMATION:
TELEPHONE: 415-655-0555
                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Lal, Freeti
APPLICANT: Guegler, Karl G.
APPLICANT: Sal, Surya K.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                   Sequence 2, Application US/08878989
Patent No. 5885803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.7%;
58.3%;
    62.9%;
54.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 58.35,
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        274 VHTPNSQKVDSQ 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: TBLYNOT01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VEVPGSQHIDSQ 12
                                                                                                     11111: 1:::
309 VEVPGAGHVEA 319
                                                                                 1 VEVPGSQHIDS 11
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: CA
                                                                                                                                                                             RESULT 22
US-08-878-989-2
                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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CURRENT FILING DATE: 1998-02-20

NUMBER OF SEQ ID NOS: 13

SEQ 1D NO 2

LENGTH: 855

TYPE: PRT

ORGANIEM: Homo sapiens

CHER INFORMATION: Amino acid sequence of TADG-15 encoded by nucleotides

OTHER INFORMATION: 23 to 2589 of Sequence 1

US-09-027-337-2
                                                                                                                                                                    Gaps
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                                                                                                                                             Score 36; DB 2; Length 855;
Pred. No. 1.4e+02;
3; Mismatches 1; Indels
                                                                                                                                              58.1%;
55.6%;
                                                                                                                                           Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 66.73
Matches 6; Conservative
                                                                                                                                                                                                   :||| :||:
370 IEVPNNQHV 378
                                                                                                                                                                                        1 VEVPGSQHI 9
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Search completed: July 16, 2001, 16:36:18 Job time: 207 sec

:|| ||||: 46 LEVDGSQHL 54

1 VEVPGSQHI 9

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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OM protein - protein search, using sw model

Run on:

July 16, 2001, 16:37:00; Search time 34.9 Seconds (without alignments) 26.192 Million cell updates/sec

US-09-786-648-3 62 Title:

1 VEVPGSQHIDSQ 12 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ស្ល	Description	cholera enterotoxi	heat-labile entero	hypothetical prote	protein F20B17.2 [hypothetical prote	(S)-2-hydroxy-acid	hippocampus-derive	carbon-monoxide de	hypothetical prote	gibberellin 20-oxi	chorismate synthas	hypothetical prote	zůotín-líke protei	hypothetical prote	probable 4-carboxy	glucarate dehydrat	probable membrane	cytochrome-c oxida	hydrolase BH3805 [methyleneterrahydr	catechol 1,2-dioxy	hypothetical prote			stress-activated p		monophenol monooxy	hypothetical prote	beta-fructofuranos
SUMMARIES	ΩI	XVVCB	QLECB	T34767	C96827	T14755	H75446	A35781	A41670	B85518	T01751	S17246	G96554	T39683	T01770	T47115	A69753	S53976	S28757	E84125	F82031	JN0143	683368	S23861	T29750	JC5694	T29029	S53529	2437	T02092
	DB	-	-	~	7	7	7	7	Н	7	7	Н	~	7	~	~	Н	~	~	~	7	~	~	7	7	~	~	7	7	7
	Length	124	124	242	260	272	353	282	674	352	367	376	423	442	550	373	455	1785	142	259	284	302	367	371	377	427	443	539	593	670
dР	Query			4	62.9	ς.	٠		61.3	59.7	59.7	59.7	59.7	59.7	59.7	58.1		58.1		56.5										56.5
	Score	62	62	40	39	39	39	38	38	37	37	37	37	37	37	36	36	36	32	32	35	32	32	35	35	35	32	32	35	35
	Result No.	н	7	က	4	S.	9	7	æ	6	10	11	12	13	14	. 15	16	17	18	19	20	21	22	23	24	25	26	27	28	53

chitin synthase (E faciogenital dyspl hypothetical prote hypothetical prote hypothetical prote hypothetical prote NADH dehydrogenase probable molybdenu hypothetical prote hypothetical prote transcription requ	probable cell divi conserved hypothet hypothetical prote
A41638 A55380 T29041 T29041 T27563 T45990 T31648 T31648 T31648 T41734 C68353	A71005 H82640 T15846
апапапапапапапа	1000
960 1258 2258 1258 181 181 252 252 269 285 285	362 398 398
Residue a control a contr	54.8
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9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4 4 4 5 4 3

# ALIGNMENTS

4		
SOLL	VCB	

Avvea

Nalernate names: enterotoxin beta chain

(Species: Vibrio cholerae

(Species: Vibrio cholerae

C; Species: Vibrio cholerae

C; Species: Vibrio cholerae

C; Species: Vibrio cholerae

C; Date: 24-Apr-1984 #sequence_revision 01-Sep-2000 #text_change 02-Feb-2001

C; Accession: S14624; S39238; S39241; H82196; JC1078; S17666; PC1010; A05130; A01819;

R; Dams, E.; de Wolf, M.; Dierick, W.

R; Dams, E.; de Wolf, M.; Dierick, W.

A; Reference number: S14623

A; Reference number: S14623

A; Residues: 1-124 - CDAN

A; Residues: 1-124 - CDAN

A; Reference number: S39238

A; Reference number: S39238

A; Residues: 1-124 - LEB>
A; Residues: 1-124 - L

A; Residues: 1-124 cLEW, A; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. Cross-references: EMBL:X76391; NID:9433859; PIDN:CAA53976.1; PID:9433861
R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. Cradafdson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; MUD:20406833
A; Accession: H82196
A; Accession: H82196
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-124 <HEI>A; AERO4224; GB:AE003852; NID:99655952; PIDN:AAF94613.1; GSPDB:GN
A; Cross-references: GB:AE04224; GB:AE003852; NID:99655952; PIDN:AAF94613.1; GSPDB:GN
A; Experimental source: serogroup 01; strain N16961; biotype El Tor
Chinese Biochem. J. 9, 395-399, 1993
A; Title: Nucleotide sequence analysis of the gene encoding the classical biotype V.ch
A; Reference number: JC1078
A; Accession: JC1078

A; Molecule type: DNA
A; Residues: 1-20, 'Q', 22-31, 'Q', 33-38, 'H', 40-49, 'G', 51-67, 'T', 69-124 <SHI>
A; Resperimental source: classical blotype strain 569B
R; Dams, E.; de Wolf, M.; Dierrick, W.
B; Dams, E.; de Blophys. Acta 1090, 139-141, 1991
A; Title: Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classic A; Reference number: S17665; MUID:9135224

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A; Molecule type: DNA
A; Residues: 1-17, 'C', 19, 'Y', 21-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-122, 'E', 124 <R
A; Residues: 1-17, 'C', 19, 'Y', 21-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-122, 'E', 124 <R
A; Residues: 1-17, 'C', 19, 'Y', 21-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-122, 'E', 124 68
A; Residues: 1-17, 'C', 19, 'Y', 21-24, 'S', 'B', 'B'
Microb. Pathog. 2, 381-390, 1987
Microb. Pathog. 2, 381-390, 1987
A; Reference number: A61475
A; Re
                                                                                                                                                                                                                                                   R;Dallas, W.S.; Falkow, S.
Nature 288, 499-501, 1980
A;Title: Amino acid sequence homology between cholera toxin and Escherichia coli heat
A;Reference number: A01820; MUID:81074965
                                                                                                                                                                                                                                                                                                                                                                                                                                             K;Yamamoto, T.; Gojobri, T.;.Yokota, T.
J. Bacteriol. 169, 1352-1357, 1987
A;Title: Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichi
A;Reference number: A26946; MUID:87137303
A;Ancession: B26946
A;Moleoni ...
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A;Residues: 1-5,/e',717,'C',19-24,'S',26-27,'E',29-33,'H',35-63,'K',65-66,'A',68-122
A;Crosx-references: GB:M/7874; NID:9145830; PIDN:AAA98064.1; PID:9145831
A;Experimental source: plasmid ENT-R PCG86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Ibrahimi, I.; Gentz, R.
J. Biol. Chem. 262, 10189-10194, 1987
A;Title: A functional interaction between the signal peptide and the translation appa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Nuclectide sequence comparison between heat-labile toxin B-subunit cistrons A;Reference number: I41194; MUID:85156481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Cross references: GB.MJ101; NID:g146375; PIDN.AAA23973.1; PID:g146376
R;Inoue, T.; Tsuji, T.; Koto, M.; Imamura, S.; Miyama, A.
FEMS Microbiol. Left. 108, 157-161, 1993
A:Title: Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic A;Reference number: 153542; MUID:93252225
                                                                                                                                    C;Species: Escherichia coli
C;Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change 18-Jun-1999
C;Accession: A01820; B26946; I41194; I41287; I67644; A61475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Molecule type: DNA
A;Residues: 1-27,'E',29-63,'K',65-124 <XAM>
A;Cross-references: EMBL:M15563; NID:g148335; PIDN:AAA24792.1; PID:g148336
R;Leong, J.; Vinal, A.C.; Dallas, W.S.
Infect. Immun. 48, 73-77, 1985
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                                                                                                   neat-labile enterotoxin chain B precursor - Escherichia coli
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0.00014;
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A;Molecule type: DNA
A;Residues: 1-22 <RE2>
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: 141287; MUID:87280041
A; Accession: 141287
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Best Local Similarity 100.0%; Pr
Matches 12; Conservative 0;
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A, Molecule type: mRNA
A, Residues: 1-124 < DAL>
R, Yamamoto, T.; Gojobori
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Almotecular type: DNA

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nes 12; Conserv
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A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-353 <WHI>
A:Cross-references: GB:AE001954; GB:AE000513; NID:g6458751; PIDN:AAF10604.1; PID:g645
A:Experimental source: strain R1
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N;Alternate names: neurotrophin-3 precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 16-Jul-1999
C;Accession: A35781; A40094
R;Ernfors, P.; Ibanez, C.F.; Ebendal, T.; Olson, L.; Persson, H.
Proc. Natl. Acad. Sci. U.S.A. 87, 5454-5458, 1990
A;Title: Molecular cloning and neurotrophic activities of a protein with structural shafefernce number: A35781; MUID:90319130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (S)-2-hydroxy-acid oxidase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C;Accession: H75446
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Wamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
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                                R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, subnitted to the Protein Sequence Database, August 1999 A;Reference number: 218181 A;Accession: T14755
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                                                                                                                                                                        A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-272 <NAM>
A;Cross-references: EMBL:AL110209
A;Experimental source: fetal brain; clone DKFZp564A0122
C;Genetics:
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Pred. No. 11;
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Pred. No. 8.3;
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66.7%;
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75.0%;
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A;Molecule type: mRNA
A;Residues: 1-282 <ERNA
A;Cross-references: GB:M34643
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Best Local Similarity
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Best Local Similarity
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246 ELPGSEHIE 254
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   C; Accession: T14755
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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Reference and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: C96827
A; Actual S. Preliminary
                                                                                                                                                                                                                                  C; Species: Streptomyces coelicolor
C; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C; Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
R; Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A; Reference number: 221556
A; Accession: T34767
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-242 AMR>
A; Residues: 1-242 AMR>
A; Cross-references: EMBL:AL031184; PIDN:CAA20190.1; GSPDB:GN00070; SCOEDB:SC2A11.21C
C; Genetics:
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A;Residues: 1-260 <STO>
A;Cross-references: GB:AE005173; NID:g7715588; PIDN:AAF68106.1; GSPDB:GN00141
C;Genetics:
A;Gene: F20B17.2
A;Map position: 1
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C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein F20817.2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.5%;
70.0%;
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50.0%;
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Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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65 VKVPGKQHVSEK 76
71 VEVPGSQHIDSQ 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||||||: | |
204 VEVPGTDHTD 213
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Best Local Similarity
Matches 6; Conserv
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R; Theologis, A.; Ec
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Gaps

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DB 2; Length 352; 27;

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Gibberallin 20-oxidase - common tobacco
Nilternate names: Ntci6 protein
C;Species: Nicotiana tabacum (common tobacco)
C;Species: Nicotiana tabacum (common tobacco)
C;Species: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 20-Jun-2000
C;Accession: T01751
R;Tanaka-Ueguchi, M.; Itoh, H.; Oyama, N.; Koshioka, M.; Matsuoka, M.
submitted to the EMBL Data Library, July 1998
A;Description: Over-expression of a tobacco homeobox gene, NTH15, decreases the expre
A;Beference number: Z14418
A;Reference number: Z14418
A;Residus: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1367 CTAN>
A;Residues: 1367 CTAN>
A;Coss;references: EMBL:AB016084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: Ntc16
C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
                                                                                                                           2; Mismatches
                                           Score 37;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37;
Pred. No. 2
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                                           59.7%;
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87.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 87.5°
                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                  320 VVVPGANHVD 329
                                           Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                   1 VEVPGSQHID 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EVPGSQHI 9
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A41670

carbon-monoxide dehydrogenase (EC 1.2.99.2) beta chain [similarity] - Clostridium therma C; Species: Clostridium thermaceticum
C; Species: Clostridium thermaceticum
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
C; Accession: A41670
R; Morton, T.A.; Raggadale, S.W.; Shanmugasundaram, T.; Wood, H.G.; Ljungd, J. Biol. Chem. 266, 23824-23828, 1991
A; Title: The primary structure of the subunits of carbon monoxide dehydrogenase/acetyl-C
A; Recession: A41670
A; Status: preliminary
A; Molicule type: DNA
A; Reterences: CB:MG2727; NID:9144784; PIDN:AAA23228.1; PID:9144785
C; Superfamily: carbon-monoxide dehydrogenase beta chain; hybrid cluster [4Fe-2S-30] homc
C; Keywords: 4Fe-2S-30, 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein; C; Keywords: 4Fe-2S-30) homcloyy <4KD.
F; 256-606/Domain: hybrid cluster (4Fe-2S-30) homoloyy <4KD.
F; 289,71,76,90/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
F; 289,731,355,470,500,550,585/Binding site: Ni-3Fe-2S-30 cluster (His, Glu, Cys, Cys, Cys, F; 470/Modified site: cysteine persulfide (Cys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B85518

"Mypothetical protein 20347 [imported] - Escherichia coli (strain 0157:H7)

"Species: Bscherichia coli

"Saccession: B85518

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

11ler, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousls, K.; Apodaca,

Nature 409, 529-533, 2001

A.Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A.Aititle: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.

A.Accession: B85518

A.Accession: B85518

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-352 <STO>

A.Residue
       Maisonpierre, P.C.; Belluscio, L.; Squinto, S.; Ip, N.Y.; Furth, M.E.; Lindsay, R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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R; Maisonpierre, P.C.; Belluscio, L.; Squinto, S.; Ip, N.Y.; Furth, M.E.; Science 247, 1446-1451, 1990
A; Title: Neurotrophin-3: a neurotrophic factor related to NGF and BDNF. A; Reference number: 440094; MUID:90208301
A; A; Accession: A40094
A; Ascideus type: DNA
A; Molecule type: DNA
A; Residues: 25-282 AMA1
A; Cross-references: GB: M33968; NID:9205771; PIDN:AAA41727.1; PID:9205772
C; Superfamily: nerve growth factor beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ó;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 282
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Pred. No. 13;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61.3%;
54.5%;
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Best Local Similarity 54.5
6. Conservative
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| VDVPGNSHTDA 11
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Best Local Similarity
Matches 6; Conserv
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1; Indels

Length 367;

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ore 37; DB; ed. No. 28; Mismatches

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Chorismate synthase (EC 4.6.1.4) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G2501; protein YGL148w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S17246; S64162
R;Jones, D.G.L.; Reusser, U.; Braus, G.H.
Mol. Microbiol. 5, 2143-2152, 1991
A;Title: Molecular cloning, characterization and analysis of the regulation of the AR A;Reference number: S17246; MUID:92114793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-376 <VOL>
A; Cross-references: EMBL:272670; NID:91322731; PIDN:CAA96860.1; PID:91322732; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-376 <JON>
A; Residues: 1-376 <JON>
A; Residues: 1-376 <JON>
A; Cross-references: EMBL:X60190; NID:93386; PIDN:CAA42745.1; PID:93387
B; Volckaert, G; Voet, M.; Verhasselt, P.; Defoor, E.
submitted to the Protein Sequence Database, May 1996
A; Reference number: S64153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.7%; Score 37; DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: chorismate synthase
C;Keywords: phosphorus-oxygen lyase; transmembrane protein
F;347-363/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross·references: SGD:S0003116; MIPS:YGL148w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:ARO2; MIPS:YGL148w
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A; Cross-references: EMBL: AF007270; NID: 92191157; PID: 92191172; GSPDB: GN00063; ATSP: A_
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C;Species: Streptomyces sp.
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glucarate dehydratase (EC 4.2.1.40) - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                               hypothetical protein A_IG002P16.9 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 22-Oct-1999 C;Accession: T01770
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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  Length 442;
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                                                                                                                                                                                                                                                                                                                                                           R.Miller, N.; Beck, C.; Kramer, J. submitted to the EMBL Data Library, June 1997 A; Description: The sequence of A. thaliana IG002P16. A; Reference number: 214421 A; Accession: T01770
  5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 2;
Pred. No. 44;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Experimental source: strain 2065
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  core 37; DB 7 red. No. 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            red. No. 44;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36;
Pred. No.
  Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-550 <MIL>
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59.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 59.7%;
Best Local Similarity 66.7%;
Matches 8; Conservative
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55.6%;
                                                 Conservative
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371 DVPSAEHVDS 380
  Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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A; Residues: 1-373 <YAN>
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225 VEIPGASHL 233
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R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Southwick, A.M.; Sun, H.; Tallon, A; Tile: Sequence and analysis of Chromosome I of the plant Arabidopsis.
A; Reference number: A86141; MUID: 21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Accession: T39683; T40195
R:Oliver, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, March 1998
A;Reference number: 221869
A;Accession: T39683
A;Accession: T39683
A;Accession: T39683
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-124 <OLI>A;Molecule type: DNA
A;Cross-references: EMBL:AL049489; PIDN:CAB39796.1; GSPDB:GN00067; SPDB:SPBC1778.01c
A;Cross-references: Extrain 972h-; cosmid c1778
A;Experimental source: strain 972h-; cosmid c1778
B;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A. submitted to the EMBL Data Library, February 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:297992; PIDN:CAB10796.1; GSPDB:GN00067; SPDB:SPBC30D10.01
A;Experimental source: strain 972h-; cosmid c30D10
C;Genetics:
A;Gene: SPDB:SPBC1778.01c; SPDB:SPBC30D10.01
A;Gene: SPDB:SPBC3D10.01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zuotin-like protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Spate: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T39683; T40195
                                                                                                                                                                                                                                                                 Species: Arabidopsis thaliana (mouse-ear cress)

Bate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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                                                                                                                                                                                                                                      hypothetical protein F19C24.16 [imported] - Arabidopsis thaliana
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A; Accession: T40195
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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Pred. No. 33;
1; Mismatches
  ed. No. 29;
Mismatches
70.0%; Pred. No.
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75.0%;
Best Local Similarity 70.0
Matches 7; Conservative
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                                                                       1 VEVPGSQHID 10
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A Molecule type: DNA
A; Residues: 1-423 <STO>
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403 VPGIQHVD 410
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A;Gene: F19C24.16
A;Map position: 1
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Length 1785;

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A; Genome: mitochondrion
A; Genetic code: SGC4
C; Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C; Keywords: copper; electron transfer; heme; magnesium; membrane-associated complex;
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                                                                                                                Score 36; DB 2; LA
Pred. No. 2.5e+02;
3; Mismatches 2;
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Pred. No. 24;
2; Mismatches
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A;Cross-references: EMBL:M83761; EMBL:M83762
C;Genetics:
                                                                                                                      58.1%;
ilarity 54.5%;
Conservative
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Similarity 60.0%;
6; Conservative
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135 VSVTGSEHLD 144
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Best Local Similarity
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Best Local Similarity
Matches 6; Conserv
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A;Molecule type: DNA
A;Residues: 1-259 <STO>
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Matches 6; Conserv
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Matches
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C; Accession: A69753

K; Kunst, F.; Ogaawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chon, S.; Enrighton, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

Nature 390, 249-256, 250

Nature 390, 240

Nature 390

Nature 39
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N;Alternate names: hypothetical protein YM9952.08
N;Alternate names: hypothetical protein YM9952.08
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 06-Feb-1998
C;Accession: S53976
A;Reference number: S53969
A;Reference number: S53969
A;Recsion: S53976
A;Residues: 1-1785 CONP
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C;Genetics:
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Pred. No. 55;
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A;Cross_references: SGD:S0004923; MIPS:YMR306w
A;Map poslition: 13R
A;Cross_references: SGD:S0004923; MIPS:YMR306w
A;Map poslition: 13R
C;Keywords: transmembrane protein
F;375-391/Domain: transmembrane #status predicted <TM1>
F;446-462/Domain: transmembrane #status predicted <TM2>
F;560-576/Domain: transmembrane #status predicted <TM3>
F;581-391/Domain: transmembrane #status predicted <TM4>
F;382-394/Domain: transmembrane #status predicted <TM6>
F;1215-1231/Domain: transmembrane #status predicted <TM6>
F;126-1231/Domain: transmembrane #status predicted <TM6>
F;1361-1377/Domain: transmembrane #status predicted <TM9>
F;1385-1401/Domain: transmembrane #status predicted <TM9>
F;1385-1401/Domain: transmembrane #status predicted <TM10>
F;1367-1523/Domain: transmembrane #status predicted <TM10>
F;1367-153/Domain: transmembrane #status predicted <TM0>
F;1367-153/Domain: transmembrane #status predicted <TM0<
F;1367-153/Do
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75.0%;
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64 EVPGGEHI 71
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Gaps

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Length 142

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A;Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BAB07524.1; GSPDB:G
A;Experimental source: strain C-125
                                                                                           R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Tille: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20263314
A;Reference number: B84125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                        C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
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- Bacillus halodurans (strain C-125)
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Pred. No. 4
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Gaps

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A,Cross-references: GB:AE004648; GB:AE004091; NID:g9948237; PIDN:AAG05606.1; GSPDB:GN
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA2218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U58752; PIDN:AAB00664.1; GSPDB:GN00022; CESP:B0218.3
A;Experimental source: strain Bristol N2; clone B0218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein B0218.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T29750
R;Woessner, J.; Wohldmann, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 4
A;Introns: 50/2; 239/1; 360/3
C;Superfamily: kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A). Cross-references: EMBL: Z14064; NID: 945366; PIDN: CAA78447.1; PID: 945369
                                                                                                                                                                                                                                                                                                                    Length 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
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A; Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 67;
2; Mismatches
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Pred. No. 68;
2; Mismatches
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85.7%; Pred. No. 69;
tive 0; Mismatches
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Best Local Similarity 62.5
Si Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-367 <STO>
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A;Molecule type: DNA
A;Residues: 1-371 <HUA>
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Matches 6; Conserv
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A; Accession: G83368
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K.; Lim,
                                                                                                                                         Ryparkhili, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel Mature 404, 50.2046, 2000

Mature 404, 50.2506, 2000

My Sol-506, 2000

My Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.

My Reference number: A81775; MUD: 20222556

My Accession: R82031

My Molecule type: DNA

My Residues: 1-284 < PARX

My Res
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R; Kivisaar, M.; Kasak, L.; Nurk, A.
Gene 98, 15-20, 1991
A; Title: Sequence of the plasmid-encoded catechol 1,2-dioxygenase-expressing gene, pheb.
A; Reference number: JN0143; MUID:91192610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd
A;Reference number: A82950; MUID:20437337
                       methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5) / methenyltetrahydrofolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cispecies: Pseudomonas aeruginosa
Cispate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
Cispate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
Cispate GB336
Ristover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Species: Pseudomonas sp.
;Date: 05-Mar-1993 #sequence_revision 05-Mar-1993 #text_change 29-Sep-1999
                                                        C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB:M57500; NID:9145127; PIDN:AAC64900.1; PID:9145129
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C;Superfamily: catechol 1,2-dioxygenase
C;Keywords: aromatic hydrocarbon catabolism; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 2;
Pred. No. 51;
4; Mismatches
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Pred. No. 54;
3; Mismatches
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Best Local Similarity 41.7%;
Matches 5; Conservative :
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Best Local Similarity 50.0
Matches 6; Conservative
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227 ISAPGHQHLTTQ 238
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A; Residues: 1-302 <KIV>
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                                                                                                                        C; Accession: F82031
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stress activated protein kinase (EC 2.7.-.-) JNKD - common carp
N.Alternate names: stress-activated protein kinase b
C.Species: Cyptinus carpio (common carp)
C.Species: Cyptinus carpio (common carp)
C.Date: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 24-Sep-1999
C.Accession: JC5694
R.Hashimoto, H.; Matsuo, Y.; Yokoyama, Y.; Toyohara, H.; Sakaguchi, M.
J. Blochem. 122, 381-386, 1997
A.Fille: Structure and expression of carp mitogen-activated protein kinases homologous t
A.Recession: JC5694
A.Status: nucleic acid sequence not shown
A.Accession: JC5694
A.Status: nucleic acid sequence not shown
A.Molecule type: mRMA
A.Residues: 1-477
C.Comment: This enzyme is a mitogen-activated protein kinase, and plays a role in egg ma
C.Comment: This enzyme is a mitogen-activated protein kinases; protein kinase homolo
C.Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C.Superfamily: protein kinase homology <KIN>
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235 PGSDHID 241
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4 PGSQHID 10 ||| ||| 226 PGSDHID 232

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STRAIN=EL TOR N16961 / SERCITYPE 01;
STRAIN=EL TOR N16961 / SERCITYPE 01;
MEDLINE-20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Elles, R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESQUENCE FROM N.A.
STRAIN=EL TOR 2125;
MEDLINE=84068199; PubMed=6646234;
Mekalanos J.J., Swartz D.J., Pearson G.D.N., Harford N., Groyne F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-1854 / 0139-BENGAL;
Yamamoto K., Do V.G.R.F., Xu M., Iida T., Miwatani T., Albert M.J.,
                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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MEDLINE-84061784; PubMed-6315707;
Lockman H., Kaper J.B.;
Lockman H., Kaper analysis of the A2 and B subunits of Vibrio cholerae enterotoxin.;
J. Biol. Chem. 258:13722-13726(1983).
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MEDLINE-94237453; PubMed-8181723;
Lebens M., Holmgren J.;
Structure and arrangement of the cholera toxin genes in Vibrio cholerae 0139.";
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to the EMBL/GenBank/DDBJ databases.
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MASP_RAT
MOB2_YEAST
ETSQ_STRCU
YAAN_BACSU
VNUC_THOGV
A37C_DROME
YOGI_CAEEL
HEM1_AGABI
PDI4_MOUSE
MAK5_YEBST
DPOL_HEMST
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Nature 306:551-557(1983).
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Dams E., de Wolf M.,
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MEDLINE-78005536; PubMed-903362;
Lai C.-Y.;
"Determination of the primary structure of cholera toxin B subunit.";
J. Biol. Chem. 252:7249-7256(1977).
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.
Fraser C.M.;
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MadDLINE-93837834, Pubmed--568472,
Abang R.G., Westbrook M.L., Westbrook E.M., Scott D.L., Otwinowski
Maulik P.R., Reed R.A., Shipley G.G.;
The 2.4 A crystal structure of cholera toxin B subunit pentamer:
choleragenoid ";
J. Mol. Biol. 251:550-562(1995).
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                                                                                                                                                                                           SEQUENCE OF 22-124.
MEDLINE-78005537; Pubmed-903363;
Kurosky A., Markel D.E., Peterson J.W.;
"Covalent structure of the beta chain of cholera enterotoxin.";
J. Biol. Chem. 252:7257-7264(1977).
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MEDLINE-94272319; PubMed-8003954;
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STRAIN-OGAWA 41 / CLASSICAL BIOTYPE;
MEDLINE-97376625; PubMed-9232653;
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EMBL; K01170; AAA27573.1; -.
EMBL; D30053; BAA06291.1; -.
EMBL; X58786; CAA41593.1; -.
EMBL; X76390; CAA5397.31; -.
EMBL; X76391; CAA5397.31; -.
EMBL; AE004224; AAF94613.1; -.
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                                                                                                                                   Nature 406:477-483(2000).
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PIR; A05130; A05130.
PIR; S14624; S14624.
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                                                                                                    cholerae
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Gaps
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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01-JAN-1990 (Rel. 13, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
HEAT-LABILE ENTEROTOXIN B CHAIN PRECURSOR (LT-B, HUMAN) (LTH-B).
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                                                                                                          CHOLERA ENTEROTOXIN, BETA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 124;
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7 AND
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100.0%; Pred. No. 7.4e-05;
M.comatches 0;
InterPro; IPR001835; -.
Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
Membrane; Enterotoxin; Signal; 3D-structure.
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MEDLINE-85156481; PubMed-3884513;
Leong J., Vinal A.C., Dallas W.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-ISOLATE H10407;
MEDLINE-83114628; PubMed-6759877;
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HEAT-LABILE ENTEROTOXIN B CHAIN PRECURSOR (LT-B, PORCINE) (LTP-B)
                                                                        Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   00
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                                Inoue T., Tsuji T., Koto M., Imamura S., Miyama A.; "Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic Escherichia coli is identical to that of human strain
                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99185101; Pubmed=10085117; Matkovic-Calogovic D., Loregian A., D'Acunto M.R., Battistutta R., Tossi A., Palu G., Zanotti G.; "Crystal structure of the B subunit of escherichia coli heat-labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enterotoxin carrying peptides with anti-herpes simplex virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 274:8764-8769(1999).
-!- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED BY THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-!- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                                                                                                                                                                                                                                                                   Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R "Identification of errors among database sequence entries and comparison of correct amino acid sequences for the heat-labile enterotoxins of Escherichia coli and Vibrio cholerae."; Mol. Microbiol. 15:1165-1167(1995).
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H10407).
CRC64;
                                                                                                                                                             STRAIN=ETEC LT 87;
Germani Y., Desperrier J.M.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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H -> Y (IN ISOLATE H
H -> R (IN ISOLATE H
4; E9F7F7C7B9D3BC47 C
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Pred. No. 7.4e-05;
                                                                                                      FEMS Microbiol. Lett. 108:157-161(1993).
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                                                                                                                                                                                                                                                      MEDLINE=95349400; PubMed=7623669;
                    MEDLINE=9325225; PubMed=8486242;
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EMBL; S60731; AAC60441.1; --
EMBL; X83966; CAA58800.1; --
PDB; 1LTR; 23-WAR-99
INTERPIO; IPR001835; --
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                   DISCUSSION OF SEQUENCE
STRAIN-ISOLATE H10407;
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                                                                                                                                            SEQUENCE FROM N.A.
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Enterotoxin;
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                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ISOLATE P307;
MEDLINE-81074965; PubMed=7003397;
Dallas W.S., Falkow S.;
"Amino acid sequence homology between cholera toxin and Escherichia coli heat-labile toxin.";
Nature 288:499-501(1980).
                                                                                                                                                                                                                                                                                                                                         MEDIINE-83156481; PubMed-3884513;
Leong J., Vinal A.C., Dallas W.S.;
"Nucleotide sequence comparison between heat-labile toxin B-subunit
cistrons from Escherichia coli of human and porcine origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ISOLATE PCG86,
MEDLINE-87137303; PubMed-3546273;
Tamamanoto T., Gojobori T., Yokota T.;
"Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichia coli and Vibrio cholerae 01.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-91238966; PubMed-2034287;
Sixma T.K., Pronk S.E., Kalk K.H., Wartna E.S., van Zanten B.A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R., "Identification of errors among database sequence entries and comparison of correct amino acid sequences for the heat-labile enterotoxins of Escherichia coli and Vibrio cholerae.";
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BEDIINE-87280041; PubMed-3301830;

Ibrahimi 1., Gentz R.;

"A functional interaction between the signal peptide and the translation apparatus is detected by the use of a single point mutation which blocks translocation across mammalian endoplasmic reticulum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sixma T.K., van Zanten B.A.M., Dauter Z., Hol W.G.J.;
"Refined structure of Escherichia coli heat-labile enterotoxin,
close relative of cholera toxin.",
J. Mol. Biol. 230:890-918(1993).
                                                                                Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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-!- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED 1
-- THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-!- SUBUNI: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
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                                                                                                                                                                                                                                                                                                                            STRAIN-ISOLATE P307;
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Gaps

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Indels

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0; Mismatches

1 VEVPGSQHIDSQ 12

ò g 124 AA.

PRT;

ELBP_ECOLI STANDARD; 1932890; P13768; P01557; 21-JUL-1986 (Rel. 01, Created)

ELBP_ECOLI RESULT

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[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                     PHOSPHOLYASE).
ARO2 OR YGL148W.
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P28777;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Morton T.A., Runquist J.A., Ragsdale S.W., Shanmugasundaram T.,
Wood H.G., Ljungdahl L.G.;
Who H.G., Ljungdahl L.G.;
"The primary structure of the subunits of carbon monoxide
dehydrogenase/acetyl-CoA synthase from Clostridium thermoaceticum.";
J. BLOL. Chem. 266:33824-23826(1991).
-i- FUNCTION: CATALYZES THE INTERCONVERSION OF CO AND COZ AND THE
SYNTHESIS OF ACETYL-COENZYME A FROM THE METHYLATED CORRINOID/IRON
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CARBON MONOXIDE DEHYDROGENASE BETA SUBUNIT (EC 1.2.99.2) (CODH).
MOORELIA thermoacetica (Clostridium thermoaceticum).
Bacteria; Firmicutes; Bacillus/Clostridium group; Moorella group;
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                                                                                                                                                                                                HEAT-LABILE ENTEROTOXIN B CHAIN.
                                                                                                                                                                                                                                                                                                                                             100.0%; Score 62; DB 1; Length 124; 100.0%; Pred. No. 7.4e-05;
                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                      6DB7DE58395EA70D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     674 AA.
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                                                                                                                                                               Pfam; PF01376; Enterotoxin_B; 1. PRINTS; PR00772; ENTEROTOXINB.
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0
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                      EMBL; M17873; AAA98065.1; -. EMBL; M15363; AAA24792.1; -.
                                         AAA23973.1; -.
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                                                                31-JAN-94.
31-JAN-94.
15-SEP-95.
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31-JAN-94.
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20-APR-95.
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                                                                                                         31-JAN-94
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                                                 A01820; QLECB.
B26946; QLECEB.
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115
124 AA;
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Matches 12; Conserv
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P27989;
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MEDLINE-97197983; PubMed-9046099;
MEDLINE-97197983; PubMed-9046099;
Voot M., Defoor E., Verhasselt P., Riles L., Robben J., Volckaert G.;
Voot M., Defoor E., Verhasselt P., Riles L., Robben J., Volckaert G.;
The sequence of a nearly unclonable 22.8 kb segment on the left arm chromosome VII from Saccharomyces cerevisiae reveals ARO2, RPL9A,
TIPL, MRFI genes and six new open reading frames.";
Yeast 13.177-182(1997).
Yeast 13.177-182(1997).
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-i- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-i- INDUCTION: BY AMINO ACID STARYNTION.
-i- SIMILARITY: BELONGS TO THE CHORISMATE SYNTHASE FAMILY.
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01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1903 (Rel. 39, Last annotation update)
CHORISMATE SYNTHASE (EC 4.6.1.4) (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
SULFUR PROTEIN, CO, AND COENZYME A. CATALYTIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                              -!- COFACTOR: NICKEL ION.
-!- SUBUNIT: TETRAMER OF TWO ALPHA AND TWO BETA CHAINS.
-!- SIMILARITY: TO R.RUBRUM CARBON MONOXIDE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductaes, Nickel; Iron-sulfur; Electron transport.
METAL 68 68 IRON-SULFUR (BY SIMILARITY).
71 71 IRON-SULFUR (BY SIMILARITY).
METAL 90 IRON-SULFUR (BY SIMILARITY).
SEQUENCE 674 Aa; 72924 MW; 54BA3D816C25F9FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Microbiol. 5:2143-2152(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92114793; PubMed-1837329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHORISMATE + ORTHOPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M62727; AAA23228.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! - COFACTOR: REDUCED FLAVIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61.3%;
54.5%;
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Best Local Similarity که ...
ایم وزیر Conservative
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379 KIPGAYHIDYQ 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A41670; A41670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EVPGSQHIDSQ 12
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SEQUENCE FROM N.A.
STRAIN=S288C;
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3238486007698C2A CRC64;

50782 MW;

455 AA;

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.;
"Determination of a 21548 bp nucleotide sequence around the 24
degrees region of the Bacillus subtilis chromosome.";
Microbiology 141:269-275(1995).
-!- FUNCTION. CATALYZES THE DEHYDRATION OF GLUCARATE TO 5-KETO-4-
DEOXY-D-GLUCARATE (5-KDGLUC) (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: D-GLUCARATE = 5-DEHYDRO-4-DEOXY-D-GLUCARATE
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-i- SIMILARITY: BELONGS TO THE MANDELATE RACEMASE / MUCONATE
LACTONIZING ENZYME FAMILY. GLUCD SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-2000 (Rel. 40, Last annoctation update)
PROBABLE GLUCARATE DEHYDRATASE (EC 4.2.1.40) (GDH) (GLUCD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.7%; Score 37; DB 1; Length 376; 70.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                           SGD; S0003116; ARO2.

SGD; S0003116; ARO2.

Pfam; PF01264; Chorismate_synt; 1.

PROSITE; PS00789; CHORISMATE_SYNTHASE_1; 1.

PROSITE; PS00789; CHORISMATE_SYNTHASE_2; 1.

PROSITE; PS00789; CHORISMATE_SYNTHASE_2; 1.

Lyase; Aromatic anino acid biosynthesis.

SEQUENCE 376 AA; 40838 MW; AF3AF65605B91E8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             455 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=168;
MEDLINE=95219079; PubMed=7704254;
                                                                                                                                                                                                                            EMBL; X60190; CAA42745.1; -. EMBL; X998G0; CAA68214.1; -. EMBL; Z72670; CAA968G0.1; -. PIR; S17246; S17246. SGD; S0003116; ARO2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; D30808; BAA06470.1; -. EMBL; Z99105; CAB12043.1; -. SubtiList; BG11161; gudD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ||||:| |
264 VSVPGSKHND 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VEVPGSQHID 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GUDH_BACSU
P42238;
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GUDH_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lyase.
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                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
--- CATALKTINTY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GALACTOSE RESIDIES IN BETA-D-GALACTOSIDES.
--- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
SUPRESSOR OF TUMORIGENICITY 14 (EC 3.4.21.-) (MATRIPTASE) (MEMBRANE-
STIPE SERINE PROTEASE 1) (MT-SP1).
STI4 OR PRSSI4 ON SNC19.
HOMO Sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thermoanaerobacter ethanolicus (Clostridium thermohydrosulfuricum). Bacteria; Firmicutes; Bacillus/Clostridium group; Thermoanaerobacter group; Thermoanaerobacter.
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153 NUCLEOPHILE (BY SIMILARITY).
85796 MW; FE011FF517E51DFC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 1; Length 743;
Pred. No. 45;
2; Mismatches 3; Indels
                        Length 455
                                                                      1; Indels
                        ;
                                                                                                                                                                                                                                                                                                                             15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
LACZ OR, LACA.
                     Score 36; DB 1
Pred. No. 26;
1; Mismatches
                                                                                                                                                                                                                                                                                      743 AA.
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PROSITE; PS00719; GLYCOSYL_HYDROL_F2_1; 1.
PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.
Hydrolase; Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                        58.1%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y08557; CAA69850.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.1%;
54.5%;
Ouery Match
Best Local Similarity 75.0
امت 6; Conservative
                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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STRAIN-ATCC 33223 / 39E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPR001649;
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Best Local Similarity
                                                                                                                                               |||| :||
64 EVPGGEHI 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1757;
                                                                                                                2 EVPGSQHI 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ST14_HUMAN
Q9Y5Y6;
                                                                                                                                                                                                                                                                                 BGAL_THEET
P77989;
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ACT_SITE
SEQUENCE
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ST14_HUMAN
                                                                                                                                                                                                                                                           BGAL_THEET
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TRANSMEM
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                                                                                                                                                                                         Lin C.Y., Anders J., Johnson M., Sang Q.A., Dickson R.B.;
"Molacular cloning of cDNA for matriptase, a matrix-degrading serine
protease with trypsin-like activity";
J. Biol. Chem. 274:18231-18236(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                            Takeuchi T., Shuman M.A., Craik C.S.;
"Reverse blochemistry: Use of macromolecular protease inhibitors to dissect complex blological processes and identify a membrane-type serine protease in epithelial cancer and normal tissue.";
Proc. Natl. Acad. Sci. U.S.A. 96:11054-11061(1999).
Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00134; TRYPSIN_HIS; 1.
PROSITE; PS00135; TRYPSIN_SER; 1.
PROSITE; PS01180; CUB, 2.
PROSITE; PS0068; LDLRA_1; 2.
PROSITE; PS50068; LDLRA_2; 4.
Signal-anchor; Glycoprotein; Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLUIAR (POTENTIAL).
CUB 1.
LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
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                                             MEDLINE-99303581; PubMed-10373424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002172; -. Pfam; PF00057; Idl_recept_a; 4. Pfam; PF00089; trypsin; 1. Pfam; PF00431; CUB; 2.
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF118224; AAD42765.2; -. EMBL; AF133086; AAF00109.1; -. HSSP; P00763; 1DPO.
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00261; LDLRECEPTOR. PRINTS; PR00722; CHYMOTRYPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000859; -.
InterPro; IPR001254; -.
InterPro; IPR001314; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      855
334
447
487
524
560
603
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                                    SEQUENCE FROM N.A.
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                    CHARACTERIZATION.
                                                                                                                                                                                     PubMed=10373425;
                  NCBI_TaxID=9606;
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214
340
452
487
5524
566
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-S288C / AB972.
STRAIN-S288C / AB972.
STRAIN-S288C / AB972.
SUBMILTED (LUTCHER C.M., BATTELL B.G., Rajandream M.A., Walsh S.V.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: UDP-GLUCOSE + (1,3-BETA-D-GLUCOSYL)(N) = UDP + (1,3-BETA-D-GLUCOSYL)(N+1).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: STRONG, TO GLSI AND GLS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
PUTATIVE 1,3-BETA-GLUCAN SYNTHASE COMPONENT (EC 2.4.1.34) (1,3-BETA-D-YMR306W OR YM9952.08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane; Transferase; Glycosyltransferase.
                                                                                                                                                                                                                                            Gaps
             CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. .) (POTENTIAL).
M. 26143132CO1F99C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                     DB 1; Length 855;
52;
                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1785 AA
                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                       Score 36;
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                   MW.
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                                                                                                                                                                                                       Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                   94769
                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
851
711
711
805
109
302
485
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4835
8952
11235
1328
1328
1414
11495
11569
1609
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                                                                                                                                                 855 AA;
                                                                                                                                                                                                                                                                                                      :||| :||:
370 IEVPNNQHV 378
                                                                                                                                                                                                                                                                                 . 1 VEVPGSQHI 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932
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1585
1655
                                                                                                                                                                                                                                                                                                                                                                                                           GLS3_YEAST
Q04952;
                 ACT_SITE
ACT_SITE
ACT_SITE
CARBOHYD
                                                                                                                CARBOHYD
                                                                                            CARBOHYD
                                                                                                                                                     SEQUENCE
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GLS3_YEAST
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RESULT 10 PHEB_PSESP

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PHEB.

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Score 35; DB 1;
Pred. No. 27;
5; Mismatches
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01-FFB-1995 (Rel. 31, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
HYPOTHETICAL PROTEIN PA2218.
   313 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEMS Microbiol. Lett. 76:267-274(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U21317; AAA62527.1; WormPep; B0495.8; CE01766. Hypothetical protein. SEQUENCE 313 AA; 36977 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                            Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 EVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 QLMGSQHVDNK 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                             NCBI_TaxID=6239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YM18_PSEAE
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YM18_PSEAE
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                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kivisaar M., Kasak L., Nurk A.; "Sequence of the plasmid-encoded catechol 1,2-dioxygenase-expressing gene, pheB, of phenol-degrading Pseudomonas sp. strain EST1001."; Gene 98:15-20(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00775; Dioxygenase; 1. PROSITE; PS00083; INTRADIOL_DIOXYGENAS; 1. Aromatic hydrocarbons catabolism; Oxidoreductase; Dioxygenase; Iron; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- CATALYTIC ACTIVITY: CATECHOL + O(2) - CIS,CIS-MUCONATE.
-1- COFACTOR: FERRIC ION.
-1- PATHWAY: PHENOL DEGRADATION.
-1- SIMILARITY: BELONGS TO THE INTRADIOL RING-CLEAVAGE DIOXYGENASE
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                                                                     Score 36; DB 1; Length 1785;
Pred. No. 1.2e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 56.5%; Score 35; DB 1; Length 302; Best Local Similarity 41.7%; Pred. No. 26; Matches 5; Conservative 3; Mismatches 4; Indels
1713 1733 POTENTIAL.
1785 AA; 207482 MW; 3475446DA46C6120 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164 IRON (BY SIMILARITY).
198 IRON (BY SIMILARITY).
222 IRON (BY SIMILARITY).
224 IRON (BY SIMILARITY).
33362 MW: A86F17E68D1EAC3A CRC64;
                                                                                                                                                                                                                                                                                                      01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CATECHOL 1,2-DIOXYGENASE (EC 1.13.11.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-91192610; Pubmed-2013408;
                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas sp. (strain EST1001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M57500; AAC64900.1; -.
                                                                     58.1%;
54.5%;
                                                                   Query Match 58.1
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Plasmid pEST1412.
Bacteria; Proteobacteria.
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : || ||: :|
227 ISAPGHQHLTTQ 238
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                                                                                                                                                                               403 EWPGAQHLSSR 413
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198
222
224
224
302 AA;
                                                                                                                                             2 EVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=306;
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P31019;
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SEQUENCE
TRANSMEM
SEQUENCE
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RESULT 11 YP68_CAEEL

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                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1 / H103;
MEDLINE-93051258; PubMed-1427017;
MHUANG H., Siehnel R.J., Bellido F., Rawling E., Hancock R.E.W.;
"Analysis of two gene regions involved in the expression of the imipenem-specific, outer membrane porin protein OprD of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kirsten J.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: SOME, TO YEAST YDL087C AND S.POMBE SPCC16A11.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 40, Last sequence update)
11-CCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 37.0 KDA PROTEIN B0495.8 IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36977 MW; 000D2327621BFED0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HD DDT TD DDT TD
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EMBL; D37929; BAA07149.1; -.
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CARBOHYD
                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                       THIOETH
                                                                                                                                 METAL
METAL
                                                                                                       METAL
                                                                                                                      METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                             INV1_MAIZE
                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cells.";
Biochim. Biophys. Acta 1261:151-154(1995).
-i- FUNCTION: THIS IS A COPRER-CONTAINING OXIDASE THAT FUNCTIONS IN
THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
COMPOUNDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN-ATCC 22788 / RIB 128;
MEDLINE-95200965; PubMed-73753;
REDITAL Y., Uraga Y., Ichishima E.;
"Molecular cloning and nucleotide sequence of the protyrosinase gene,"
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Aspergillus oryzae.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOPAQUINONE + H(2)0.
COFACTOR: BINDS TWO COPPER IONS.
ENZYME REGULATION: ACTIVATED BY ACIDIFYING TREATMENT AT PH 3.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                melO, from Aspergillus oryzae and expression of the gene in yeast
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: L-TYROSINE + L-DOPA + O(2) - L-DOPA +
"Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                       56.5%; Score 35; DB 1; Length 371; 62.5%; Pred. No. 32; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                          R -> P (IN REF. 1).
R -> P (IN REF. 1).
A -> G (IN REF. 1).
D7EBOCCAC95A7CF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TYROSINASE (EC 1.14.18.1) (MONOPHENOL MONOOXYGENASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBUNIT: HOMOTETRAMER.
-i- PTM: THE N-TERMINAL IS BLOCKED.
-i- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     539 AA.
                                                                                                                                                                     EMBL; Z14064; CAA78447.1; -.
EMBL; AE004648; AAG05606.1; ALT_INIT.
            opportunistic pathogen.";
Nature 406:959-964(2000).
-1- SIMILARITY: TO E.COLI YCJY.
                                                                                                                                                                                                                                                                  40840 MW;
                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                      261
                                                                                                                                                                                               PIR; S23861; S23861.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    343 VPGASHVD 350
                                                                                                                                                                                                                                                                                                                                                            3 VPGSQHID 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYRO_ASPOR
Q00234;
                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYRO_ASPOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 33, Last sequence update)
(Rel. 35, Last annotation update)
UTRANOSIDASE 1 PRECURSOR (EC 3.2.1.26) (SUCROSE-6-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;
Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CV. B73;

MEDLINE-95357417; Pubmed=7630946;

Xu J., Pemberton G.H., Almira E.C., McCarty D.R., Koch K.E.;

Xu J., Pemberton G.H., Almira E.C., McCarty D.R., Koch K.E.;

"The Ivr 1 gene for invertase in maize.";

Plant Physiol. 108:1293-1294(1995).

-!- CATALTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.

-!- SUBCELLULAR LOCATION: VACUOLAR.

-!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BETA-FRUCTOFURANOSIDASE 1.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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Pred. No. 49;
                                                                                                                                                                                                              i) Oxidoreductase; Monooxygenase; Copies A (BY SIMILARITY).

84 COPPER A (BY SIMILARITY).

93 COPPER B (BY SIMILARITY).

290 COPPER B (BY SIMILARITY).

294 COPPER B (BY SIMILARITY).

393 COPPER B (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001362; -- Property Program Processes and Program Processes and Processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD2ECD702A018E15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY
InterPro; IPR00227;
Pfam; PF00264; tyrosinase; 2.
PRONTS; PR00092; TYROSINASE.
PROSITE; PS00497; TYROSINASE_1; 1.
PROSITE; PS00499; TYROSINASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYDROLASE 1) (INVERTASE 1).
                                                                                                                                                                                                                                                          63
84
93
290
294
333
84
60604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BETA-FRUCTOFURANOSIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 670
139
165
                                                                                                                                                                                                                       Melanin biosynthesis;
METAL 63
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294
333
333
82
539 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Glycos
Multigene family.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays (Maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-4577;
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165
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P49175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996
01-NOV-1997
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Best_Local Similarity
Matches 6; Conserv
     || || || || || || PGDQHDDAQ 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 PGSQHIDS 11
                                                                                                                                                             FGD1_MOUSE
P52734;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZN_FING
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
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                                                                                                         RESULT 16
FGD1_MOUSE
                                24
                                                                                                                                                                  ALD DE REPORTE DE LA DESTRE DE LA DESTRETA DE LA DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PLASMA MEMBRANE.
-1- SUBCELLULAR LOCATION: 1 THE CHITIN SYNTHASE FAMILY. SUBFAMILY CLASS
                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92090722; PubMed-1836444;
Yarden O., Yanofsky C.;
"Chitin synthase I plays a major role in cell wall biogenesis in Neurospora crassa.";
Genes Dev. 5:2420-2430(1991).
-!- FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.
-!- FUNCTION: PLAYS A MAJOR ROLE IN CELL WALL BIOGENESIS.
-!- CATALYTIC ACTIVITY: UDP-N-ACETYL-D-GLUCOSAMINE + [1,4-(N-ACETYL-BETA-D-BETA-D-BETA-D-GLUCOSAMINYL)](N) = UDP + [1,4-(N-ACETYL-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BETA-D-BE
                           (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CHITIN SYMWHASE 3 (EC 2.4.1.16) (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 3) (CLASS-III CHITIN SYNTHASE 3).
        (POTENTIAL)
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002923; -.
Pfam; PF01644; Chitin_synth; 1.
Transferase; Glycosyltransferase; Transmembrane; Cell wall;
                                                                                                                                                                                     DB 1; Length 670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 960; 92;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
N-LINKED (GLCNAC. .) (POT W; DEDE0989C7E6AEBO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   633A2107319BF447 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             960 AA
                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                   Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                         71932 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.5%;
                                                                                                                                                                                   56.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M73437; AAA33568.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106903
                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            591
650
685
737
765
867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLUCOSAMINYL)](N+1)
                                                                                                                                                                                                                                                                                       1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                     61 VTVLASQHVDGQ 72
275
518
595
639
670 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A41638; A41638
                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHS3_NEUCR
P29070;
                                                   CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
  CARBOHYD
                                CARBOHYD
                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
CHS3_NEUCR
                                                                                                                                                                                                                                   Matches
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4 PGSQHIDSQ 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dyspiasia (Fgd1) gene.";

Mamn. Genome 6:658-651(1995).

-!- FUNCTION: ACTIVATES THE RAS-LIKE FAMILY OF RHO- AND RAC PROTEINS

BY EXCHANGING BOUND GDP FOR FREE GTP.

-!- SUBCELLUAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-!- SIMILARITY: CONTAINS 1 DBL-HOMOLOGY DOWAIN (DH).

-!- SIMILARITY: CONTAINS 2 PH DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                        [1]
MEDLINE-96081343; PubMed-8535076;
MEDLINE-96081343; PubMed-8535076;
Pasteris N.G., de Gouyon B., Cadle A.B., Campbell K., Herman G.E.,
                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PUTATIVE RHO/RAC GUARLER UNCLECHIDE EXCHANGE FACTOR (RHO/RAC GEF)
(FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).
                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gorski J.L.;
"Cloning and regional localization of the mouse faciogenital
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 960;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41C1B84DE490FC51 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO-RICH. SH3-BINDING (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guanine-nucleotide releasing factor; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB 1;
Pred. No. 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     961 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00621; RhoGEF; 1.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
PROSITE; PS50003; PH_DOMAIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C2H2-TYPE.
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD, MGI:104566; Fgd1.
interPro; IPR0000319; -
InterPro; IPR000812; -
InterPro; IPR001849; -
Ffam; PF01363; FYVE; 1.
Pfam; PF01363; FYVE; 1.
Pfam; PF00163; PH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
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STANDARD;
                                                                                                                                                                                                                         Mus musculus (Mouse).
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820
960 AA;
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FGD1_HUMAN
ID FGD1_HUMAN
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                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-98232498; PubMed-9564035;
Inobara N., Koseki T., Chen S., Wu X., Nunez G.;
"CIDE, a novel family of cell death activators with homology to the 45 kba subunit of the DNA fragmentation factor.";
EMBO J. 17:2526-2533(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-20083488: Pubmed=10617198; Murphy G., Volckaert G., Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesterhoeft A., Stickema W., Entian K.-D., Terryn N., Harris B., Ansorge W., Brandt P., Grivell L., Rieger M., Weichselgartner M., de Simone V., Obermaier B., Mache R., Waeller M., Kreis M., Delseny M., Puigdomener, P., Watson M., Schmidtheini T., Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE 24 KDA SUBUNIT PRECURSOR (EC 1.6.5.3)
                                          01-OCT-2000 (Rel. 40, Created)
1-OCT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
CELL DEATH ACTIVATOR CIDE-A (CELL DEATH-INDUCING DFFA-LIKE EFFECTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Wakaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.8%; Score 34; DB 1; Length 219; 71.4%; Pred. No. 28; 1.4%; Pred. No. 28; 1.1ve 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 CLUE-N.
24686 MW; 05F704823CE71C0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 AA
                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: ACLIANAL.
-!- SUBUNIT: INHIBITED BY DFFB.
-!- SIMILARITY: CONTAINS 1 CIDE-N DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                   -! - FUNCTION: ACTIVATES APOPTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF041378; AAC34987.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02017; CIDE-N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
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  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EC 1.6.99.3).
AT4G02580 OR T10P11.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33 1
219 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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109 MPGSQHV 115
                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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CIDA_HUMAN
060543;
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O22769;
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                                                                                                                                                          CIDEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: FACIOGENITAL DYSPLASIA (AARSKOG-SCOTT SYNDROME) IS A RARE MULTISYSTEMIC DISORDER CHARACTERIZED BY DISPROPORTIONATELY SHORT STATURE, AND BY FACIAL, SKEEFTAL, AND URGENITAL ANOMALIES.
SIMILARITY: CONTAINS 1 DEL-HOMOLOGY DOMAIN (DH).
SIMILARITY: CONTAINS 2 PH DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: CYPOLASMIC (BY SIMILARITY).

TISSUE SPECIFICITY: FFALL HEART, BRAIN, LUNG, KIDNEY, PLACENTA,
AND LESS IN LIVER; ADULT HEART, BRAIN, LUNG, SKELETAL MUSCLE, AND
LESS IN PAROREAS AND LIVER.
                                                                                                                                                                                                                                                                                                        MEDLINE-95042764; PubMed-7954831;
Pasteris N.G., Cadle A., Logie L.J., Porteous M.E.M., Schwartz C.E., Stevenson R.E., Glover T.W., Wilroy R.S., Gorski J.L.;
"Isolation and characterization of the faciogenital dysplasia (Aarskog-Scott syndrome) gene: a putative Rho/Rac guanine nucleotide exchange factor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell 79:669-678(1994).
-!- FUNCTION: ACTIVATES THE RAS-LIKE FAMILY OF RHO- AND RAC PROTEINS
BY EXCHANGING BOUND GDP FOR FREE GTP.
                  01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence.update)
01-OCT-2000 (Rel. 40, Last annotation update)
PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF)
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Guanine-nucleotide releasing factor; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 1;
Pred. No. 92;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1. PROSITE; PS50003; PH_DOMAIN; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO-RICH.
                                                                                                             (FACIOGENITAL DYSPLASIA PROTEIN)
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75.0%;
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InterPro; IPR000306; ...
InterPro; IPR00082; ...
InterPro; IPR001849; ...
Pfam; PF01363; FYVE; I...
Pfam; PF00169; PH; 2...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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758
921
                                                                                                                                                       Homo sapiens (Human).
                                                                                                                                                                                                                                                                                          TISSUE-Craniofacial;
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590
734
821
961 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                           NCBI_TaxID=9606;
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SEQUENCE
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CIDA_HUMAN

RESULT

Matches

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Gaps

IRON-SULFUR (2FE-2S) (POTENTIAL). 27C95BF5884B12AC CRC64;

11

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RA Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA Jangham S.-A., McCullagh B., Bilham L., Robben J., Vandenbussche F.,
RA Ger Schueran J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA Mitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzer E., Brandt A., Peters S., Van Staveren M., Dirkee W.,
RA Holzer E., Brandt A., Peters S., Van Staveren M., Intree W.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA Bertett A., Bugsbaert J., Kay M., Lennard N., McLay K.,
RA Glark L., Doggett J., Hall S., Kay M., Lennard N., McLay K.,
RA Borkva D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkva D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkva D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkva D., Bloecker H., Schaffer M., Roenes V., Rechmann S.,
Ra Borkva D., Bloecker M., Schaffer M., Casacuberta E.,
RA Gabel C., Fruchs M., Partmann B., Granderath K., Dauner D., Herzl A.,
RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Felber R.,
Ra Andenber S., Hiller R., Schmidt W., Lecharny A., Racon D., Josse T.,
RA Berz-Perez A., Purnelle B., Bent E., Johnson S., Taccon D., Josse T.,
Ra Fibman D., Haase D., Lemcke K., Mewes H. W., Stocker S.,
Ra Fibman D., Bente B., Bent E., Johnson S., Raccaria P., Bertley J., Sheet P., Cordes M., Abu-Threideh J.,
Rateralle D., Dedhia W., Wilson R.K., Mewes R., Borkon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
Rameralle D., Chiller P., Haber S., Gerkel K., Johnson D.,
RA Kramer J., Bentley D., Fulton B., Miller N., Greco T., Layman D.,
Rameralle M., Martiss E., Dante M., Mahuray J., Sheet P., Cordes M., Abu-Threideh J.,
Rameralle M., Martiss B., Vander M., Merchoulu B., Zidanto M., Stroker S.,
Ratteralle P., Courtrow W., Villon B., Miller N., Greco T., Emper S., Sho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THALLING TO THE RESPIRATORY

1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE BUXZME IS BELIEVED
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE BUXZME IS BELIEVED
TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
FRAGMENT OF THE ENZYME (BY SIMILARITY).

1- COPALATITE ACTIVITY: NADH + UBIQUINONE - NAD(+) + UBIQUINOL.

1- COPACTOR: 2FE-2S IRON-SULFUR CLUSTER N 1B (BY SIMILARITY).

1- SUBGNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
THIS IS A COMPONENT OF THE FLAVOPROPEIASMIC SIDE OF THE
MITOCHONDRIAL INNER MEMBRANE (BY SIMILARITY).

1- SIMILARITY: BELONGS TO THE COMPLEX I 24 KDA SUBUNIT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MITOCHONDRION (POTENTIAL)
NADH-UBIQUINONE OXIDOREDUCTASE 24 KDA SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01257; complex1_24kD; 1.
PROSITE; PS01099; COMPLEX1_24K; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AC002330; AAC78260.1; -. EMBL; AL161494; CAB80751.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002023; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fron-sulfur.
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IRON-SULFUR (2FE-2S) (POTENTIAL). IRON-SULFUR (2FE-2S) (POTENTIAL). IRON-SULFUR (2FE-2S) (POTENTIAL).

119 124 160

244

CHAIN METAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                    "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBL_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 1; Length 365;
Pred. No. 49;
4; Mismatches 2; Indels
                                                          Length 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0423; CELLDVISFTSZ.
PRINTS; PR01161; TUBULIN.
PROSITE; PS00227; TUBULIN: 1.
Cell division; Septation; GTP-binding; Multigene family.
NP_BIND
99 107 GTP (POTENITAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 structure and evolution."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NP_BIND 99 107 GTP (POTENTIAL)
SEQUENCE 365 AA, 39957 MW; ACC31761552F0CC5 CRC64;
                                                         Score 34; DB 1;
Pred. No. 31;
                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                          365 AA.
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                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                            CELL DIVISION PROTEIN FTSZ HOMOLOG 3. FTSZ3 OR PAB1820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL DIVISION PROTEIN FTSZ HOMOLOG 3. FTSZ3 OR PH1335.
 164 IF
27182 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ248285; CAB49728.1; -. InterPro; IPR000158; -. InterPro; IPR000217; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FT23_PYRHO STANDARD; F 059060; 01-0CT-2000 (Rel. 40, Created)
                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.8%;
45.5%;
                                                         54.8%;
                                                         Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 45.5
Matches 5; Conservative
                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyrococcus horikoshii.
                                                                                                                                                                                                                                                    01-OCT-2000 (Rel. 40, 01-OCT-2000 (Rel. 40, 01-OCT-2000 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (Rel. 40, 01-OCT-2000 (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::||| | :|:
195 IDVPGEQTLDA 205
164 1/
244 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VEVPGSQHIDS 11
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                              Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=29292;
                                                                                                                    4 PGSQHIDS 11
                                                                                                                                     STRAIN-ORSAY;
                                                                                                                                                                                                                        FTZ3_PYRAB
                                                                                                                                                                                                                                                                                                                                                                                                                      Heilig R.;
 METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                         Q9V0H5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FESULT 21
FTZ3_PYRHO
AC 05906.0.
DT 01-0CT
DT 01-0CT
DT 01-0CT
DE CELL DC
GN FTSZ3 (0)
CO AFCEO
OX NCBL_T
                                                                                                                                                                                           RESULT 20
FTZ3_PYRAB
   SO
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SUBCELLULAR LOCATION: NUCLEAR.
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                                                                                                                                                                                                                                                                                                                                        Developmental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 23
AROC_NEUCR
ID AROC_NEUCR
AC Q12640;
                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                             Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Osuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.; Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Trrcheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

BEDILINE-967212167; PubMed-8670808;
Hahn M., Jackle H.;

"Drosophila goosecoid participates in neural development but not in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  body axis formation.";
EMBO J. 15:3077-3084(1996).
-!- FUNCTION: APPEARS TO REGULATE REGIONAL DEVELOPMENT OF SPECIFIC
TISSUES. CAN RESCUE AXIS POLARITY IN UV-RADIATED XENOPUS
                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ς;
                                                                                                                                                                                                                                                                                                                                                                                                 54.8%; Score 34; DB 1; Length 365; 45.5%; Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goriely A., Stella M., Coffinier C., Kessler D., Mailhos Dessain S., Desplan C.;
                                                                                                                                                                                                                                                                                                                                    Septation; GTP-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                GTP (POTENTIAL).
; DC987E91C761F5B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                functional homologue of goosecoid in Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HOMEOBOX PROPEIN GOOSECOID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     419 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 49;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                 MEDLINE-98344137; PubMed-9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Embryo;
MEDLINE-96202483; PubMed-8625850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Development 122:1641-1650(1996).
                                                                                                                                                                                                                                                                       EMBL; AP000006; BAA30441.1; -.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 365 AA; 40118 MW;
                                                                                                                                                                                                                                                                                                                     PROSITE, PS00227; TUBULIN;
Cell division; Septation: G
                                                                                                                                                                                                                                                                                                             Pfam; PF00091; tubulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                  InterPro; IPR000217;
InterPro; IPR003008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::||| | :|:
195 IDVPGEQTLDA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VEVPGSQHIDS 11
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBRYOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSC_DROME
P54366;
                                                                                                                                                                                                                                                                                                                                                NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
TISSUE SPECIFICITY: IN EARLY EMBRYO DEVELOPMENT, EXPRESSION CONFINED TO TWO REGIONS, A HORSESHOR-LIKE PATPERN ACROSS THE DORSAL SIDE WHICH IS DESTINED TO FORM THE BRAIN HEMISPHERES AND A SECOND DOMAIN WHICH INVAGINATES INSIDE THE STOMODEUM AND WHICH, IS
                                                                                                                                                              SYSTEM (SNS).
--- SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEOBOX PROTEINS.
"BLCOLD" SUBFAMILY.
--- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: 5-0-(1-CARBOXYVINYL)-3-PHOSPHOSHIKIMATE -
CHORISMATE + ORTHOPHOSPHATE.
COFACTOR: REDUCED FLAVIN.
PATHMAX: SEVENTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                           FATED TO FORM THE FOREGUT, RING GLAND AND STOMATOGASTRIC NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHORISMATE SYNTHASE (EC 4.6.1.4) (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. Chem. 270:20447-20452(1995).
-!- FUNCTION: BIFUNCTIONAL ENZYME THAT POSSESSES CHORISMATE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND INTRINSIC FLAVIN REDUCTASE ACTIVITY, IT USES NADPH TO REDUCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bifunctional chorismate synthase/flavin reductase from Neurospora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; Nuclear protein; DNA-binding; Homeobox.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99386486; PubMed-7657620;
Henstrand J.M., Amrhein N., Schmid J.;
"Cloning and characterization of a heterologously expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Length 419;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         851A4C46AA861FB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB
Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44949 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.8%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X95420; CAA64699.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U52968; AAB17948.1; -.
HSSP; P06601; 1FJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            homeobox; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0010323; Gsc.
InterPro; IPR001356; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169
199
345
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286
3
419 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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DOMAIN
CARBOHYD
  PROSITE;
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                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                   IL7R_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
  ETT FT FT SO
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                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NATURE 407:508-513(2000).

-I FUNCTION: BINDS TO THE SIGNAL SEQUENCE OF PRESECRETORY PROTEIN WHEN THEY EMERGE FROM THE RIBOSOMES (BY SIMILARITY).

-I SUBUNIT: ARCHARAL SIGNAL RECCGNITION PARTICLE CONSISTS OF A 7S RNA MOLECULE OF 300 NUCLEOTIDES AND TWO PROTEIN SUBUNITS: SRP54 AND SRP19 (BY SIMILARITY).

-I SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-I SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

-I DOMAIN: HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE 75 RNA IN PRESENCE OF SRP19 AND ALSO BINDS THE
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL SEQUENCE (BY SIMILARITY). SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                           ó
                                                                                                                                      EMBL; U25818; AAC49056.1; -.
InterPro; IPR000453; -.
Pfam; PP01264; Chorismate_synt; 1.
PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.
PROSITE; PS00788; CHORISMATE_SYNTHASE_2; 1.
PROSITE; PS00789; CHORISMATE_SYNTHASE_2; 1.
Lyase; Aromatic amino acid biosynthesis; Oxidoreductase; NADP; Multifunctional enzyme.
NP_BIND 260 291 NADPH (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae; Thermoplasma
                                                                                                                                                                                                                                                                                                            54.8%; Score 34; DB 1; Length 432; 77.8%; Pred. No. 59;
SIMILARITY: BELONGS TO THE CHORISMATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                      NADPH (POTENTIAL).
201A0B525C406F0C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
SIGNAL RECOGNITION 54 KDA PROTEIN (SRP54).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456 AA
                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-DSM 1728;
MEDLINE-20479972; PubMed-11029001;
                                                                                                                                                                                                                                                                      432 AA; 45967 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL445064; CAC11655.1; -.
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 77.0-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermoplasma acidophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                     274 EVPGSIHND 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEOUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    2 EVPGSQHID 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRP54 OR TA0515
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SR54_THEAC
ID SR54_THEAC
AC Q9HKT0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acidophilum.
                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-90199875; Pubmed-2317865;
Goodwin R.G., Friend D., Ziegler S.F., Jerzy R., Falk B.A.,
Gimpel S., Cosman D., Dower S.K., March C.J., Namen A.E., Park L.S.;
"Cloning of the human and murine interleukin-7 receptors:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i - FUNCTION: RECEPTOR FOR INTERLEUKIN-7.
-i - SUBUNIT: HETERODIMER OF AN ALPHA CHAIN AND A COMMON GAMMA CHAIN.
-i - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i - TISSUE SPECIFICITY: SPLEEN; THYMUS; AND FETAL LIVER.
-i - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-i - SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SER/THR-RICH.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERLEUKIN-7 RECEPTOR ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSO1355; HEMATOPO_REC_S_F1; 1. ; Transmembrane; Glycoprotein; Phosphorylation; Signal.
                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    demonstration of a soluble form and homology to a new receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-AUG-1990 (Rel. 15, Created)
1-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INTERLEUKIN-7 RECEPTOR ALPHA CHAIN PRECURSOR (IL-7R-ALPHA).
                                                                                                                                                                                                                                                     Length 456;
                  Darticle; GTP-binding; RNA-binding.
289 G-DOMAIN (BY SIMILARITY).
456 M-DOMAIN (BY SIMILARITY).
111 GTP (BY SIMILARITY).
188 GTP (BY SIMILARITY).
245 GTP (BY SIMILARITY).
545 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                Score 34; DB 1;
Pred. No. 62;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M29697; AAA39304.1; -. PIR; D34791; D34791.
                                                                                                                                                                                                                                                  54.8%;
75.0%;
  SRP54; 1.
                                                                                                                                                                                                                                                  Query Match 54.8
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001777; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:96562; 117r.
Interpro; IPR000950; -.
Interpro; IPR001777; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      459
239
264
459
225
189
60
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                         Signal recognition
                                                                                                                                                                            456 AA;
PS00300;
                                                                                                                                                                                                                                                                                                                                                                                 353 IPGSOKID 360
                                                                                                                                                                                                                                                                                                                                                    3 VPGSQHID 10
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104
184
242
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PROSITE; PS0135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                superfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL7R_MOUSE
P16872;
                                                                     DOMAIN
NP_BIND
NP_BIND
NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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ó;
 115 115 N-LINKED (GLCNAC. ..) (POTENTIAL).
177 N-LINKED (GLCNAC. ..) (POTENTIAL).
282 282 PHOSPHORYLATION (BY PRC) (POTENTIAL).
459 AA; 51704 MW; CC06A5CE95543849 CRC64;
CARBOHYD
CARBOHYD
MOD_RES
SEQUENCE
 FT
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0; Gaps Query Match 54.8%; Score 34; DB 1; Length 459; Best Local Similarity 66.7%; Pred. No. 63; Matches 6; Conservative 2; Mismatches 1; Indels 1 VEVPGSQHI 9. :|| ||||: 46 LEVDGSQHL 54

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Search completed: July 16, 2001, 16:44:03 Job time: 462 sec

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Oghas on capient ogyans ogyans ogyans streptomyce ogyans terspromyce ogyans lepsamania oges26 helicoverpa oges26 helicoverpa ogyans hepatitis b ogyans hepatitis ha ogy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95303036; PubMed-7783690;
Nakashima K., Eguchi Y., Nakasone N.;
"Characterization of an enterotoxin produced by Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Microbiol. Immunol. 39:87-94(1995).
HSSP; P01556; 1XTC.
InterPro; IPR001835; -.
Pfam: PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTERCIOXINB.
SEQUENCE 103 AA; 11645 MW; 992A05C077F2F70E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   057193.
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERA TOXIN B PROTEIN (CTB) PRECURSOR (CTB).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERA-LIKE ENTEROTOXIN B SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                         09E226
09S079
09S079
09S079
09DUH5
09DUH1
091529
09DUH1
091520
097704
099V9U6
095V9U6
095V9U6
095V9U6
095V9U6
095V9U6
004636
Q9HB36
Q9XD79
Q9V7M7
Q9U0W5
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042099
001797
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Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
1 VEVPGSQHIDSQ 12
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SEQUENCE.
  09R646;
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ID 05 AC 05 DT 011 DT 01 DT 01 DT DT DT DT DT DT DT DE CH
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Q9R646
  AC
DDT TO DD TO DD
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Q57193 vibrio chol
Q5653 vibrio chol
Q9r015 vibrio chol
Q9r015 vibrio chol
Q9r025 streptomyce
Q3135 bacillus ce
Q3nqq6 homo sapien
Q9rjz8 streptomyce
Q9mal6 arabidopsis
Q9uq04 homo sapien
Q9ry17 deinococcus
Q9ry17 deinococcus
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014347 schizosacch
080418 nicotiana t
099987 homo sapien
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O22511 vitis vinif
                                                                                                                                                                        July 16, 2001, 16:43:36; Search time 57.41 Seconds (without alignments) 27.655 Million cell updates/sec
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                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           425026 seqs, 132305027 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  protein search, using sw model
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Q9RP15
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Q99987
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
sp_vertebrate:*
sp_virus:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_phage:*
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Maximum DB seq length: 2000000000
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62
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Match Length DB
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Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SINGUENCE FROM N.A.
STRAIN-Y, CN BW SP;
MEDLINE-99403001; PubMed-10471707;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Harris N., Harrizell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
Celniker S., Rubin G.M.;
An exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster: the Adh region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shin H.J., Park Y.C., Kim Y.C.;
Shin H.J., Park Y.C., Kim Y.C.;
"Cloning and nucleotide sequence analysis of the virulence gene cassette from Vibrio cholerae KNIH002 isolated in Korea.";
Misainmurhag Haiji 35:205-210(1999).
EMBL: AFI/5708; AAD51360.1; -.
HSSP; P01556; 2CHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 62; DB 2; Length 124; Best Local Similarity 100.0%; Pred. No. 0.00037; Matches 12; Conservative 0; Mismatches 0; Indels
                                                          Length 124;
                                                                                                 0; Indels
13871 MW; 3F87B2F297953179 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001835; -.
Pfam; PF01376; EnterOtoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
SEQUENCE 124 AA; 13905 MW; 23BF83FFF793E5B9 CRC64;
                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERA ENTEROTOXIN B-SUBUNII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last anhotation update)
HYPOTHETICAL 43.6 KDA PROTEIN.
BG:DS0154.3.
                                                   Query Match
100.0%; Score 62; DB 2; I
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 12; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                    124 AA
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                                                                                                                                                                 71 VEVPGSQHIDSQ 82
                                                                                                                                           1 VEVPGSQHIDSQ 12
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    124 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae.
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Q9RP15;
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                                                                                               SEQUENCE FROM N.A.
STRAIN-CLASSICAL STRAIN 569B;
MEDLINE-9135224; PubMed-1883840;
MEDLINE-913524; De Wolf M., Dierick W.;
"Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classical strain 569B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Comparison of cholera toxin genes (ctxAB) of non-01 vibrio cholerae strains 854 (0139-bengal) and S7 (037) from two outbreaks."; Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases. HSSP: D01556; 2CHB.
                               Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
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Yamamoto K., Do V.G., Xu M., Iida T., Miwatani T., Albert M.J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 62; DB 2; Length 124; 100.0%; Pred. No. 0.00037; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                    Xu L.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X58785; CAA41591.1; -.
EMBL; U25679; AAC34728.1; -.
EMBL; A00931; CAA00098.1; -.
HSSP; P01556; ZCHB.
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Last sequence update)
Last annotation update)
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Shi C., Cao C., Zhang J., Ma Q.;
Chin. Biochem. J. 9:395-399(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001835; -. Pfam; PF01376; Enterotoxin_B; 1. PRINTS; PR00772; ENTEROTOXINB.
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Pfan; PP01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
PRODOM; PD012805; -; 1.
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124 AA; 13919 MW;
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STRAIN=CLASSICAL BIOTYPE 569B;
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Best Local Similarity
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  CTXB.
Vibrio cholerae.
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Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
Lehrach H., Poustka A., Lundeberg J.;
"The European IMAGE consortium for integrated Molecular analysis of
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                 STRAIN*ATCC 10987;
Kolsto A.B., Okstad O.A., Lindback T., Hegna I., Lagreid A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 62.9%; Score 39; DB 4; Length 192; Best Local Similarity 66.7%; Pred. No. 12; Matches 6; Conservative 3; Mismatches 0; Indels
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y11217; CAA72103.1; -.
InterPro; IRR000212; -.
Pfam; PF00580; UvrD-helicase; 1.
PNON_TER 1 1
NON_TER 24 29212 MW; 24392E11338D99EA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL389957; CAB97531.1; -.
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                                                                                                                       031335,
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OGT-2000 (TrEMBLrel. 15, Last annotation update)
ATP-DEPENDENT NUCLEASE SUBUNIT A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
LLPL, LCAT-LIKE LYSOPHOSPHOLIPASE (FRAGMENT).
                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus. NCBI_TaxID=1396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 2;
Pred. No. 11;
2; Mismatches
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58.3%;
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Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 IDEPGSQHIRKQ 46
    204 VEVPGTDHTD 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 EVPGSQHID 10
                                                                                                                                                                                                                                             Bacillus cereus.
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SEQUENCE
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09NPQ6;
                                                                                                       031335
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                                                               RESULT
031335
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                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

CALNIKAT S.E., Adpayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Calnikat S.E., Adpayani A., Chavez C., Chew M., Cicsiolka L., Doyle C.M.,
Butenhoff C., Champe M., Chavez C., Chew M., Cicsiolka L., Doyle C.M.,
Ratfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
Nixon K., Pacleb J.M., Park S., Pfelffer B., Poon L., Sequeira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
Zieran L.L., Rubin G.M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003408; AAF44847.1;
Riyase, FSHO0028907; BG:DS01514.3.

Riyase, FSHO0028907; BG:DS01514.3.
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL031184; CAA20190.1;
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Pred. No. 4.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy L., Harris D.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2);
Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002502; --
Pfam, PF01510; Amidase_2; 1.
Hypothetical protein.
SEQUENCE 242 AA; 26018 MW; 6DD10FF18A2EC544 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) HYPOTHETICAL 26.0 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                    69.4%;
Genetics 153:179-219(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 64.5
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         330 VSVPGSTHIDA 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VEVPGSQHIDS 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=1902;
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0.086 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1. 10 1.

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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Cheuk R., Shinn P., Brooks S., Buehler E., Chiou J., Chol E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Lil J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, ACO10793; AAF68106.1; -. ERGURE Z60 AA; 29128 MW; B149F22073AA0B92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases. EMBL, ALI10209; CABS3675.1; -. InterPro: IPR03386; -. Fram: PF02450; LACT; I. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
 1."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                          Ecker J.R.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                  Ecker J.R.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31016 MW; ACCC5E1680D7A720 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Last sequence update) 01-WAR-2001 (TrEMBLrel. 16, Last annotation update) HYPOTHETICAL 31.0 KDA PROTEIN.
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Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 10;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 4; Pred. No. 18; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.9%;
50.0%;
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Q9RVJ7;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 62.9
Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al protein.
272 AA; 31
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65 VKVPGKQHVSEK 76
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SEQUENCE FROM N.A.
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                                                                                                                             SEQUENCE FROM N.A.
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246 ELPGSEHIE 254
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ID Q
AC Q
DT 0
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"A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor A3(2) chromosome.";
MMOI. MICTODIOI. 21:77-96(1996).
EMBL, AL133210; CAB61584.1;
InterPro. IPR002502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic sequence for Arabidopsis thaliana BAC F20B17 from chromosome
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Eukaryota: Viridiplantae: Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,
Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E.,
Conway A., Gorales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
Ecker J.R.;
                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces. NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 2; Length 201;
Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-A3(2);
Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                       STRAIN=A3(2);
Oliver K., Harris D.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01510; Amidase_2; 1.
SEQUENCE 201 AA; 22749 MW; B8EF477E06A20468 CRC64;
                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
F20B17.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 AA.
                                                                                            201 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                 Created)
                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
                                                                                                                             01-MAY 2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14, PUTATIVE AMIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.9%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.9
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                            PRELIMINARY;
                                                                                                                                                                                                                         Streptomyces coelicolor.
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
166 ELPGSEHIE 174
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 EVPGSDHTD 184
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Q9MA16;
                                                                                                               09RJZ8;
                                                                                          Q9RJZ8
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Q9RJZ8
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EMBL; AF019907; AAB70837.1; -.
HSSP; P00390; 1ALG.
Mendel, 26381; VItvi;1190;26381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.9%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         022511;
01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-MAR-2001 (TrEMBLrel. 16,
                                                               01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 63.6
Matches 7; Conservative
                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vitis vinifera (Grape).
                                                                                                          ESTS AU056822(S20908).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EVPGSQHIDSQ 12
                                                                                                                         Oryza sativa (Rice)
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                           NCBI_TaxID=4530;
                                                                                                                                                                                                                                                             clone: P0041E11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                        Q9LGM2;
Q9LGM2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             022511
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022511
               14
               RESULT
                               O9LGM2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                  MEDLINE=20036896; PubMed=10567266; White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
NCBL_TaxID=1299;
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MEDLINE-99194552; PubMed=10092508;
Taniyama Y., Shibata S., Kita S., Horikoshi K., Shirafuji H.,
Sumino Y., Fujino M.;
"Cloning and expression of a novel lysophospholipase which
structurally resembles lecithin cholesterol acyltransferase.";
Biochem. Biophys. Res. Commun. 257:50-56(1999).
EMBL; AB017494; BAA76877.1; -.
InterPro; IRRO03386; -.
Pfam; PPC0450; LACT; 1.
SEQUENCE 412 AA; 46657 MW; IFEA8A5783AF050A CRC64;
                                                                                                                                                                                                                               "Genome sequence of the radioresistant bacterium Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                    62.9%; Score 39; DB 2; Length 353; 75.0%; Pred. No. 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62.9%; Score 39; DB 4; Length 412; 66.7%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                INCEFFIC, LEANCECT,
PEONIC PROJUCTO, FMN_ALD, 1.
PROSITE; PS00557; FMN_HYDROXY_ACID_DH; 1.
SROHFRICE 353 AA; 37877 MW; 14FB78FABZE18C8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
LCAT-LIKE PROTEIN (LLPL).
  Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              412 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 24;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 28;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                    Science 286:1571-1577(1999).
EMBL; AE001954; AAF10604.1;
HSSP; P05414; 1GOX.
01-MAR-2001 (TrEMBLrel. 16, (S)-2-HYDROXY-ACID OXIDASE.
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 62.9
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                              InterPro; IPR000262; -. InterPro; IPR003009; -.
                                          Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|||:||:
386 ELPGSEHIE 394
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 EVPGSQHID 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 VPGSEHLD 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 VPGSQHID 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                             radiodurans R1
                                                                                                                                                                                                                    Fraser C.M.;
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Gaps
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Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; Vitis.
NCBI_TaxID=29760;
                                                                           Eukaryota, Viridipiantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta; Liliopsida, Poales; Poaceae, Ehrhartoideae, Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. THOMPSON SEEDLESS (CLONE 2A); TISSUE-FRUIT;
Cassol I., Adams D.O.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
--- COPACTOR: FAD (BY SIMILARITY).
--- SIMILARITY: TO PYRIDINE NUCLEOTIDE-DISULPHIDE OXIDOREDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                SEQUENCE FROM N.A.
STRANH=CV. NIPPONBARE;
SASAKI T., MATSUMOTO T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 10; Length 428; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                             "Oryza sattvu ...errordon Colone: P0433F93."

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AP002521; BAA96762.1; -.
EMBL; AP002539; BAB08201.1; -.
InterPro; IPR001552; -.
Pfam; PF00441; Acyl-CoA_dh; 1.
PR05TIE; PS00073; ACYL_COA_DH_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUTATHIONE REDUCTASE (NADPH) (EC 1.6.4.2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000103; -.
InterPro; IPR001100; -.
InterPro; IPR001327; -.
Pfam; PF00070; pyr_redox; 1.
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RESULT 17
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RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.F.,
RA Gamatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Gacrge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beaaley E.M.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kanison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kunison J.A., Ketchum K.A.,
RA Jalali M., Murphy B., Murphy L., Mornis J., Noshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson R., Nelson K.A., Naxon K., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Shilt T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chan H.Y.E., Harris S.J., O'Kane C.J.; Identification and characterization of kraken, a gene encoding a putative hydrolytic enzyme in Drosophila melanogaster."; Gene 222:195-201(1998).
                                                                                                                                                                   Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                      DB 10; Length 565;
                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
PROBABLE SERINE HYDROLASE (EC 3.1.-.-) (KRAKEN PROTEIN).
PRINTS; PR00368; FADPNR.
PRINTS; PR00411; PNDEDTASEI.
PRINTS; PR00469; PUNDEDTASEII.
PROSTITE; PS00076; PYRIDINE_REDOX_1; 1.
FAD; Flavoprotein; Oxidoreductase; Redox-active center.
                                                                                         565 AA; 60695 MW; B26113AE09A121DE CRC64;
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                                                                                                                                                                                                                                                                                                    331 AA
                                                                                                                                     62.1%; Score 38.5; 172.7%; Pred. No. 48;
                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
                                                                                                                                                                                                                                                                                                    PRT;
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MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99051329; PubMed-9831651;
                                                                                                                                   Query Match 62.1
Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                           239 EIPGSEHAIDS 249
                                                                                                                                                                                              2 EVPGSQH-IDS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                         KRAKEN OR CG3943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ephydroidea; Dro
NCBI_TaxID-7227;
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01-MAR-2001
                                                                          NON_TER
SEQUENCE
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   SO RY ES
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weisenbach J.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang G., Zhao Q., Zhao G., Zha
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Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: Z-DAB BINDING PROTEIN. COULD BE INVOLVED IN CHROMOSOME ORGANIZATION (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN.
EMBL. 297992; CABI0796.1; -.
HSSP: P25685; 1HDJ.
InterPro: IPR001623; -.
Pfam; PF00226; DnaJ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2YGOTICALLY.
SIMILARITY: WEAK, TO FAMILY OF ESTERASES THAT GROUPS TOGETHER
PSEUDOMONA TROPINESTERASE, DMPD; TODF AND XYLF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 BY SIMILARITY.
37093 MW; 1FE39BC42AED4E69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) PUTATIVE ZUOTIN-LIKE PROTEIN C30D10.01 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.7%; Score 37; DB 66.7%; Pred. No. 52; tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-1998 (TrEMBLrel. 06, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00561; abhydrolase; 1.
PROSITE; PS00120; LIPASE_SER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 60...
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 VEVPGTHHL 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VEVPGSQHI 9
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SEQUENCE
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004636;
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004636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; Core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Troh H., Oyama N., Koshioka M., Matsuoka M.; anaka-Ueguchi M., Itoh H., Oyama N., Koshioka M., Matsuoka M.; "Over-expression of a tobacco homeobox gene, NTH15, decreases the expression of a gibberellin biosynthetic gene encoding GA 20-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Butheria, Primates, Catarrhini, Hominidae, Homo.
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PROSITE; PS00636; DNAJ_1; 1.
PROSITE; PS50076; DNAJ_2; 1.
SMART; SM00271; DnaJ; 1.
Hypothetical protein; Chaperone; DNA-binding; Nuclear protein.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 59.7%; Score 37; DB 10; Length 367; Best Local Similarity 87.5%; Pred. No. 58; Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                           Score 37; DB 3; Length 354;
Pred. No. 56;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases EMBL, AB010084; BAA31690.1; -. Mendel, 31081. Nicta;2972;31081.
                                                                                                           DNAJ-LIKE.
ALA/LYS-RICH.
; 6071B58A3B60F558 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam, PF00671; Fe_Asc_oxidored; 1.
SEQUENCE 367 AA; 42170 MW; 923BC90B3BBBAC05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAY-1997 (TIEMBLrel. 03, Created)
01-JAN-1998 (TFEMBLrel. 05, Last sequence update)
01-WAR-2001 (TFEMBLrel. 16, Last annotation update)
VRK2, COMPLETE CDS.
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TISSUE-LIVER;
MEDLINE-98008921; PubMed=9344656;
Nezu J., Oku A., Jones M.H., Shimane M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                           40290 MW;
                                                                                                                                                                                                                           59.7%;
50.0%;
                                                                                                                                                                                                                                                                       5; Conservative
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                                                                                                                  81
                                                                                                                                      267
                                                                                                             10
217
354 AA;
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283 DVPSAEHVDS 292
                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 5; Conserv
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NTC16.
                                                                                                                                    DOMAIN
SEQUENCE
                                                                                                                    DOMAIN
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080418
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099987
AC 099987
DT 01-7AN DT 01-7AN DT 01-7AN DT 01-7AN DT 01-7AN DT 01-7AN DE VREZ, OS HOMD SOC MAMMA1 OC NAMMA1 CO NAMMA1 DR NELINERR RA MEDLIN RA NEZU 19
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"Identification of two novel human putative serine/threonine kinases, VRK1 and VRK2, with structural similarity to vaccinia virus B1R
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01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MDL-1997 (TrEMBLrel. 16, Last sequence update)
SIMILARITY TO GATA-TYPE ZINC FINGERS.
A_IGO02P16. 9.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; endicocyledons; core endicots; Rosidae; eurosids II; NCBI_TAXID=3702;
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                                                                                                                                                                                         PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
SMART; SM00220; S_TKC; 1.
ATP-binding; Serine/threonine-protein kinase; Transferase.
SEQUENCE 508 AA; 58126 MW; 157FBF6F48511AF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Length 508
                                                             Genonics 45:327-331(1997).
-!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL, AB000450; BAA19109.1; -.
HSSP: Q06486; DICK.
InterPro; IPR000719; -.
InterPro; IPR0002290; -.
                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
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STRAIN-CV. COLUMBIA;
Miller N., Beck C., Kramer J.;
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (101-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF007270; AAB61058.1; -
Mendel; 17174; Arath;2663;17174.
InterPro; 178000679; -
Pfam; PF00320; GATA; 1.
PROSITE; PS50114; GATA, ZN_FINGER_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00401; ZnF_GATA; 1.
SEQUENCE 550 AA; 60856 MW; 488A05F20846091D CRC64;
                                                                                                                                                                                                                                                                                                                                                                          Score 37; DB 4;
Pred. No. 82;
1; Mismatches
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Pred. No. 90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9HB36 PRELIMINARY; PRT;
Q9HB36;
01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                                                                            59.7%;
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Best Local Similarity bo...
8; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 VHTPNSQKVDSQ 345
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SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Waterston R.;
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Admanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Rad Admanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Rad George R.A., Learis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Button G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
R. Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
R. Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
R. Abril J.F., Benos P.V., Berman B.P., Bhandari D., Bolshakoy S.,
R. Borkova D., Botchan M.R., Boute J., Barckstein P., Brotkter P.,
R. Borkova D., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
R. Borkova D., Bolcher A., Deng C., Mays A.D., Dew I., Dietz S.M.,
R. Borkova D., Bolcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
R. Bortis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
R. Cabliellan A.E., Carroll J.H., Gu Z., Gunn P., Harris M.,
R. Dodson K., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Dodson K., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R. Hortin D., Houston K.A., Hehman T.J., Hernandez J.R., Houck J.,
R. Hostin D., Houston K.A., Hehman T.J., Hernandez J.R., Houck J.,
R. Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
R. Alalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Mosherson D.,
R. Matteil B., McIntcsh T.C., McLeod M.P., McPherson D.,
R. Matteil B., McIntcsh T.C., McLeod M.P., McPherson D.,
R. Merkulov G., Milshina N.V., Mobarry C., Morris J., Puri V., Reese M.G.,
R. Alangson K., Dalson K., Sunges R.D.C., Scheeler F., Shen H.,
R. Spier E., Spradling A.C., Stapleton M., Stupski M.P., Snith T.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Snith T.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Snith T.,
Spier E., Spradling A.C., Stapleton M., Stupski W. W., Williams C., Turner R., Walner E., Wang A.H., Wallston R.,
Shillan S., Marylor R., Walner C., Wallston R., Wallston R.,
Shillan S., Rainer R., Walner R., Walner R., Walner R., Walner R., Wa
                                                                                                                                                                                                                      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 382;
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                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CG7750 PROTEIN.
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0900W5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
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54.5%;
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348 ELPGPQHKETO 358
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
   : 7M7V60
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ID Q9
AC Q9
DT 01
      DDT TE THE TEACH TO THE TEACH TO THE TEACH TO THE TEACH TO THE TEACH THE THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE TEACH THE T
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                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBL_TaxID=86383;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last aentotation update)
4-CARBOXYMUCONOLACTONE DECARBOXYLASE/3-OXOADIPATE ENOL-LACTONE
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

Cao J., Fan W., Zheng S.;

Gao J., Fan W., Zheng S.;

Genomic analysis of a novel human serine protease SNC19.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF283256; AAG13949.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 4; Length 325;
Pred. No. 79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 2; Length 373;
Pred. No. 92;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
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-!- SIMILARITY: TO ALPHA/BETA HYDROLASE FOLD.
EMBL; AF109386; AAD40815.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35896 MW; F6A7468C1B26B64F CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                            SERINE PROTEASE SNC19 (FRAGMENT).
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PRINTS; PR00111; ABHYDROLASE.
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Best Local Similarity 55.0.
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Best Local Similarity 55.6
Matches 5; Conservative
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"Genetic organization of Helicoverpa zea nuclear polyhedrosis virus in "Genetic organization of Helicoverpa zea nuclear polyhedrosis virus in the region of EcoRI U.D.L.A and Q.";
Submitted (JUN.2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF275264; AAG17375.1;
SEQUENCE 527 AA; 59935 MW; ElDF20478A77574C CRC64;
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                                                Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
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MEDLINE-98146435; PubMed=9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 58.1%; Score 36; DB 14; Length 527; Best Local Similarity 54.5%; Pred. No. 1.3e+02; Matches 6; Conservative 3; Mismatches 2; Indels
                                                                                                                                STRAIN=FRIEDLIN;
Jamesrman W., Wambutt R., Ivens A.C., Murphy L., Quail M.,
Rajandream M.A., Barrell B.G.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                              "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
BMBL; ALI33436; CabaC2821.1; -.
Hypothetical protein.
SEQUENCE 389 AA; 42733 MW; 4C1AOCF31D0DC670 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.1%; Score 36; DB 5; Length 389; Best Local Similarity 66.7%; Pred, No. 96; Matches 1; Indels Matches 1; Indels
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| 107 PGARHIDVQ 115
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Q9E226
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July 16, 2001, 16:35:41; Search time 56.06 Seconds (without alignments) 22.710 Million cell updates/sec | SIDS8/gcgdata/geneseqp/An1991_DAT:
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Maximum DB seq length: 2000000000 A_Geneseq_0601:* US-09-786-648-4 111: 112: 114: 116: 117: 118: 118: 118: 120: .. Perfect score: Scoring table: Database: Sequence: Searched: Run on: Title:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Cholera toxin B/en	Synthetic cholera	Heat labile entero	Cholera toxin B su	Cholera toxin B su	Amino acid sequenc	Cholera Toxin B-su	B subunit of the h	Cholera toxin B su	Amino acid sequenc	Plant-optimized E.
	ID	AAY87462	AAW04857	AAR94939	AAW06606	AAW06607	AAW80808	AAR04163	AAP93561	AAW06605	AAW59770	AAY96652
	DB	21	17	17	17	17	19	11	10	17	19	21
	Query Match Length DB	21	103	103	103	103	103	118	124	124	124	124
фP	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	106	106	106	106	106	106	106	106	106	106	106
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LTB-CTB fusion pro Sequence of LT-B-M LTB-CTP fusion pro HSV-1 antigen/heat Sequence of sub-un	E. coli heat labil ADP-ribosylating t Escherichia coli v E. coli heat-labil Heat labila toxin E. coli verotoxin-l	Recombinant exotox Recombinant exotox Recombinant exotox Recombinant exotox Labile toxin (LT-B	C. jejuni flagelli Plant-optimized V. GtfB.1/CTB chimeri B subunit of CT. Adhesin/V.cholerae Helicobacter pylor Helicobacter pylor	Sequence of amino Network polymer wh Network polymer wh Adhesin/CTXA2B chi Sequence of amino.	Cholera toxin B an Cholera toxin B an Residues 50-64 of Cholera toxin B/en Cholera toxin B/en Cholera toxin B su Bovine rotavirus V
AARO4825 AAR50227 AAW94082 AAR11272 AAP50340	AAY87463 AAR72545 AAY41816 AAW95226 AAY68365	AAB73241 AAB73242 AAB73243 AAB73244 AAY01300	AAW67443 AAY96872 AAR12630 AAR28831 AAW80599 AAW80699	AAP30600 AAP50436 AAP50439 AAY32094 AAP30265	AAP93498 AAR85125 AAR76748 AAY87461 AAB15525
11 15 20 12 6	20 20 21 20 21 20 21	22222	122 123 13 13 13 13 13 13 13 13 13 13 13 13 13	40004	10 16 21 21 21 21
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12 13 14 15	17 18 20 21 21	23 25 27 27	. 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		4 4 4 4 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6

## ALIGNMENTS

Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:4. AAY87462 standard; peptide; 21 AA. 03-JUL-2000 (first entry) AAY87462; AAY87462

RESULT

Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta 4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.

Vibrio cholerae. Escherichia coli 

WO200014114-A1.

16-MAR-2000.

99WO-GB02970. 07-SEP-1999;

98GB-0019484.

07-SEP-1998;

(UYBR-) UNIV BRISTOL.

Williams NA, Hirst TR;

WPI; 2000-256943/22.

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor GM-1.

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or may not be of Bordetella origin, can be used for the expression in Bordetella of enzymes, antiques, immunogens, allergens, enzyme inhibitors, hormones, lymphokines, immunogens, allergens, enzyme inhibitors, hormones, lymphokines, immunogens, allergens, enzyme inhibitors, hormones, lymphokines, immunogenila or their fragments, toxins, mammalian proteins, structural proteins or receptors. The Bordetella strains are particularly engineered to express the cholera toxin B subunit (this sequence). The promoters used in the constructs are selected from the Bordetella pertussis toxin subunit si leader (SI-L) and the pertussis toxin subunit SI leader (SI-L) and the pertussin pertactin cleader (PRN-L); and genes used in the constructs are selected from the cholera toxin B leader (CTB-L), the pertussis toxin subunit SI leader (SI-L) and the pertussin pertactin cleader (PRN-L); and genes used in the constructs are selected from a novel synthetic cholera toxin B gene (ctb) and the hmwl and hmw2
                                                                                                                                                                                                                                 Recombinant constructs comprising a promoter functional in Bordetella operatively linked to a heterologous gene or a non-Bordetella leader sequence for secretion of a gene product which may
                                                            Example 1; Figure 1; 61pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GATFQVEVPGSQHIDSQKKAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
\overset{\mathbf{x}}{\mathbf{a}}\overset{\mathbf{x}}{\mathbf{a}}\overset{\mathbf{x}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset{\mathbf{y}}{\mathbf{a}}\overset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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composed of one A subunity control of the composed of one A subunity and five feet of one A subunity and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB) activity, while the B subunits (EtxB and CtxB) activity of GM-I receptors. Although GM-I binding is responsible for some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-I binding. The peptides of the invention are fragments of the beta-4-alpha-2 loop of EtxB and CtxB, exerting the same effects as normal EtxB and CtxB, such as nimmunomodulator or adjuvant. They may be used as an inhibitor for toxin-induced diarrhoea.

Therefore, the peptides may be used in the production of a composition of or treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced disease associated with an immune disorder and/or toxin-induced disease sasociated with an immune disorder and/or toxin-induced disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                         The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 106; DB 21;
100.0%; Pred. No. 2.7e-11;
ive 0; Mismatches 0;
                                                                     Disclosure; Page 15; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW04857 standard; Protein; 103 AA
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Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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Gaps

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Length 103; Indels

Score 106; DB 17; Pred. No. 1.7e-10; Mismatches 0;

ö 100.0%; 100.0%;

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A transgenic plant comprising or expressing a DNA sequence encoding an immunogenic agent can be be used as an oral vaccine for animals. The vaccine is administered by the oral consumption of the plant and provides the first known functional method for immunising animals
                                                                                                                                                                                                                                                                                                                                                                                               Transgenic plants contg. E. coli heat labile enterotoxin subunits used as oral vaccines for animals which consume the plant
                                                                                                         Toxin; subunit; vaccine; transgenic plant; immunogen; antigen;
                                                                               Heat labile enterotoxin B subunit (LT-B) E.coli.
                                                                                                                                                                                                                                                                                                                            Mason HS;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 100-101; 130pp; English.
AAR94939 standard; Protein; 103 AA.
                                                                                                                                                                                                                                                                                                                            Hag TA,
                                                                                                                                                                                                                                                                                                  (TEXA ) UNIV TEXAS A & M SYSTEM.
                                                                                                                                                                                                                                                                                   (TULA ) TULANE EDUCATIONAL FUND
                                                                                                                                                                                                                                95WO-US13376.
                                                                                                                                                                                                                                                         94US-0328716.
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT18799, AAT18800
                                                    (first entry)
                                                                                                                                                                                                                                                                                                                            Clements JD,
                                                                                                                          adjuvant; immunisation
                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-230602/23.
                                                                                                                                                  Escherichia coli.
                                                                                                                                                                          WO9612801-A1.
                                                                                                                                                                                                                                24-OCT-1995;
                                                                                                                                                                                                                                                         24-OCT-1994;
                                                                                                                                                                                                                                                                                                                             Arntzen CJ,
                                                                                                                                                                                                     02-MAY-1996.
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cholera toxin B subunit; enzyme; antigen; immunogen; allergen; enzyme inhibitor; hormone; lymphokine; immunoglobulin; toxin; structural protein; receptor; heterologous gene; leader; promoter.

Bordetella pertussis; whooping cough; recombinant construct;

Synthetic cholera toxin B subunit.

(first entry)

21-FEB-1997

ò 요 Recombinant constructs for expressing and opt. secreting proteins in Bordetella - comprise Bordetella promoter coupled to non-Bordetella, esp. cholera B toxin, gene or coupled to non-Bordetella leader and

Zealey GR;

Klein MH, Loosmore SM, Yacoob RK,

WPI; 1996-425088/42.

N-PSDB; AAT38038.

gene of interest

(CONN-) CONNAUGHT LAB LTD.

23-FEB-1995; 23-FEB-1996; 29-AUG-1996

96WO-CA00107. 95US-039334

WO9626282-A1

Synthetic.

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AAW06607
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using transgenic plants, where the plants express bacterial antigens that act as both immunogens and adjuvants. The method provides an inexpensive production and delivery system for such antigens to animals. This is the LT-B Escherichia coli toxin subunit and its coding sequence was used in the construction of such a transgenic plant. The immunogenic agent preferably comprises the LT-B or CT-B (cholera toxin B subunit) or optionally LT-A or CT-A.
                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                         Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; CTB; heat labile enterotoxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea; vomiting; food poisoning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW06606 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein,
                                                                                                                                                                                                                                                                                     Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                  ;
0
                                                                                                               Length 103;
                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "wild-type Ala replaced by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                            /label= substitution
/note= "wild-type Thr replaced by Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "wild-type His replaced by Asn"
                                                                                                             100.0%; Score 106; DB 17;
100.0%; Pred. No. 1.7e-10;
ive 0; Mismatches 0;

    Vibrio cholerae.
    Enterotoxigenic Escherichia Coli.

                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= substitution
                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                           AAW06606 standard; Protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page -; 32pp; English.
                                                                                                                                                     1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                45 gatfgvevpgsghidsgkkai 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-SE00570
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                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                       Local Similarity 100. nes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Holmgren J, Lebens MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-506108/50.
N-PSDB; AAT43576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R.
                                                                                 103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
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                                                                                                                                                                                                                                                                                                                                                            Chimeric
Chimeric
                                                                                  Sequence
                                                                                                              Query Match
                                                                                                                                                                                                                                             AAW06606
                                                                                                                         Best Loca
Matches
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Gaps
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certain amino acids (aa) were replaced with corresponding aa from heat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.

Note - This sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see AAW06605).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 1..25
/label= substitution
/label= "the first 25 amino acids of mature
/note= "the first 25 amino acids of mature
wild-type cholera toxin B subunit are
replaced with the first 25 amino acids
of mature enterotoxin B subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 106; DB 17;
100.0%; Pred. No. 1.7e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric - Vibrio cholerae.
Chimeric - Enterotoxigenic Escherichia Coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW06607 standard; Protein; 103 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-SE00570.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vomiting; food poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Holmgren J, Lebens MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-506108/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R.
                                                                                                                                                                                                                                                                                                                                                                                                           103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT43577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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enables the possibility for commercial mucosal adjuvants for use in humans, since these are more effective and safer than vaccines administered subcutaneously.

103 AA;

Sequence

SSSSSS

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AAW06607 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding as from theat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.

C and vomiting, in humans and animals.

C and vomiting, in sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera toxin B subunit; nontoxic subunit; adjuvant; coadministration; antigen; bird; animal; mucosal; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of the cholera toxin B subunit used in the method of the invention involving the use of nontoxic subunits as an effective adjuvant in coadministration of an antigen to birds and animals. In addition to the use of the toxin as am mucosal adjuvant, it also provides a vaccine comprising the toxin, an immunogenic amount of an antigen, and a pharmaceutically acceptable carrier. The toxin can be used with single/multiple vaccines, and it
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New mutant cholera toxin selected from a group comprising nontoxic subunits/derivatives - effective as an adjuvant when coadministered with an antigen to birds and mammals
                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                             Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of the wild type chorela toxin B subunit.
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                             100.0%; Score 106; DB 17; 100.0%; Pred. No. 1.7e-10;
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                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW80808 standard; protein; 103 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takeda Y,
                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                               21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UAB RES FOUND
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TAKEDA Y.
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (YAMA/) YAMAMOTO S.
                                                                                                                                                                                                                                                            103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (KIYO/) KIYONO H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09845324-A1
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                                                                                                                                                                                                                             AAW06605).
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                                                                                                                                                                                                                                                              Seguence
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                                                                                                                                                                                                         cholera toxin B-subunit; hybrid protein; heterologous IgA active antigen.
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                        Gaps
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 Length 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New hybrid protein, useful in vaccines - contains cholera toxin b subunit and heterologous \ensuremath{\mathsf{IgA}} active
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                   1..11
/*label= signal peptide
/*note= absent from mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 11;
Score 106; DB 19;
Pred. No. 1.7e-10;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 106; DB 11;
llarity 100.0%; Pred. No. 2e-10;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                            18..18
/*label= His or Tyr
                                                                                                                    AAR04163 standard; protein; 118 AA.
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 21; Conservative 0;
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                                           1 GATFQVEVPGSQHIDSQKKAI 21
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                                                      45 gatfqvevpgsqhidsqkkai
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                                                                                                                                                                                     Cholera Toxin B-subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1990-132273/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigenic sequence.
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les 21; Conserv
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                                                                                                                                                                                                                                                         misc_difference
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                                                                                                                                                                                                                             synthetic.
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                                                                                                                                          AAR04163;
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AAP93561;

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RESULT

Pept1de Protein

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AAW06605 is the full (including the signal peptide) length cholera toxin B subunit (CTB), this sequence is described as unpublished in the specification. The mature CTB protein was used to create hybrid mutants, in which certain amino acids (aa) of CTB were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB), see AAW06605 and AAW06607. The specific amino acids substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic lillness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.
                Cholera toxin B subunit, used for hybrid immunogenic toxin production.
                                             Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; CTB; heat labile enterotoxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea; comiting; food poisoning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
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100.0%; Pred. No. 2.2e-10;
tive 0; Mismatches 0;
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/label= sig_peptide
22..124
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/label= mat_protein
                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1; 32pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Holmgren J, Lebens MR;
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Matches 21; Conserv
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                                                                                                                                      Vibrio cholerae
                                                                                                                                                                                                                                                                               WO9634893-A1
                                                                                                                                                                                                                                                                                                                                                   02-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                      (LEBE/) 1
                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                            Protein
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                                                                                                                                                     B subunit of the heat-labile enterotoxin (LT-B) derived from E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                      B subunit; heat-labile enterotoxin; LT-B; Escherichia coli; malari circumsporozoite protein; fusion protein; live recombinant vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   comprising attenuated entero-invasive bacterium contg. DNA encoding epitope of malaria parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 106; DB 10;
Pred. No. 2.2e-10;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hockmeyer WT;
                                                                                                                                                                                                                                                                                                                           /note="Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Live recombinant vaccine for malaria
                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     /note="Mature LT-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW06605 standard; Protein; 124 AA.
                                             AAP93561 standard; protein; 124 AA.
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100.0%;
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Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1989-114399/15.
                                                                                                                                                                                                                          Salmonella; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 AA;
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                                                                                                                                                                                                                                                               coli.
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                                                                                                                  06-JUN-1990
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                                                                                                                                                                                                                                                             Escherichia
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Length 124; Indels

Seguence

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AAW06605

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WO200037609-A2
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                                      22-DEC-1999;
                    29-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral;
                                                                                                                                                                                                                                                                      This is the amino acid sequence of Escherichia coli beta-subunit of heat labile enteritoxin (LTB). It is used in the method of the invention to create fusion proteins which are useful as vaccinating immunogens. The fusion proteins are useful in vaccines, specifically where the antigenic peptide is an inhibin fragment for increasing the fertility of an animal (by increasing levels of follicle stimulating hormone (FSH) or production of sperm or ova), but more generally for inducing an immune response against the antigenic peptide. Vaccines are particularly administered orally, e.g. fusion protein is expressed in edible plants or animals.
Beta-subunit of heat labile enterotoxin; LTB; fusion protein; vaccine; immunogen; antigen; inhibin; fertility; follicle stimulating hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                   New nucleic acid encoding fusion of antigenic peptide and enterotoxin sub-unit - useful as vaccinating immunogen, particularly for increasing animal fertility by inducing antibodies against inhibin
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100.0%; Pred. No. 2.2e-10;
iive 0; Mismatches 0;
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/label- signal_peptide
22..124
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/label= mature_protein
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                                                                                                                                                                                                                                                       Disclosure; Fig 9; 56pp; English.
                   FSH; sperm; ova; immune response.
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                                                                                                                   96US-0747410.
                                                                                                                                     (UNMS ) UNIV MICHIGAN STATE
                                                                                                                                                         Bagdasarian M, Ireland J;
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Best Local Similarity 100.0
Matches 21, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adjuvant; anti-bacterial
                                                                                                                                                                           WPI; 1998-297947/26.
N-PSDB; AAV41573.
                                                                                                                                                                                                                                                                                                                                                                                   124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
Synthetic.
                                       Escherichia coli.
                                                        WO9821344-A1
                                                                                                                   12-NOV-1996;
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                                                                             22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY96652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY96652
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This synthetic Escherichia coli heat-labile toxin (LT) B subunit (LT-B) is encoded by a plant-codon optimized CDNA. The CDNA sequence contains plant-preferred codons and eliminates sequence motific associated with spurious mRNA processing. The second codon is changed from AAT encoding Asn to GTG encoding Val, in order to create a NcoI restriction site at the 5' end. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide or a which have reduced enzyma activity as compared to the wild-type LT-A or polypeptide and where at least one of the codons is altered to a coll and preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the polynucleotides in transgenic plants to produce edible vaccines, especially cral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 106; DB 21;
100.0%; Pred. No. 2.2e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'label-first AA of mature LTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23..24
/label-AAs encoded by linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..21
/label=LTB leader sequence
                                                                                                                                      (BOYC-) BOYCE THOMPSON INST PLANT RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cholera toxin; diarrhoea; enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR04825 standard; protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 5A-B; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 gatfqvevpgsqhidsqkkai 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio cholreae serogroup 01
99WO-US30747
                                                                     98US-0113507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          also useful as adjuvants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTB-CTB fusion protein.
                                                                                                                                                                                                                                                                                 Mason HS, Arntzen CJ;
                                                                                                                                                                              (MASO/) MASON H S.
(ARNT/) ARNTZEN C J.
                                                                                                                                                                                                                                                                                                                                               WPI; 2000-442653/38.
N-PSDB; AAA51156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 AA;
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Self-tolerance; fusion protein; immune response; LTB; CTP; hCG; cancer; labile toxin subunit B; carboxy terminal peptide; prophylaxis; fertility; human chorionic gonadotrophin; LTB-CTP.
                                                                                                                                                                                                                                                                                                                                                                                                                   The surface M protein of Group A streptococi is the major virulence factor and protective antigen of these organisms. However, there are a tremendous number of M protein serotypes. The invention provides recombinant M protein antigens comprising a gene encoding a carrier protein and an NH2 or COOH terminal M protein fragment carrying one or more epitcopes. The carrier may be the B subunit of E.coll labile toxin (LT-B). The carrier and the antigen may be linked by a linker, eg AAR50226. The LT-B-M24 fusion gene of the example was expressed using E.coll. The M24 component constists of a pair of synthetic oligos which copied the first 36 bp of the emm 24 gene. Rabbits immunised with the LT-B-W24 developed type-specific bacteriocidal antibodies against type 24 streptococci.
                                                                                                                                                                                                                                                                                                                New recombinant hybrid streptococcal M protein antigen(s) - which elicit opsonic antibodies without eliciting cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 106; DB 15;
100.0%; Pred. No. 2.4e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "LTB protein"
125..133
/note= "linker peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                    antibodies to mammalian heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "LTB protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW94082 standard; Protein; 170 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08; FL
                                                                                                                                                                                          (UYTE-) UNIV TENNESSEE RES CORP
                                                                                                                                                                                                                                                                                                                                                                                     Example; Fig 1; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66 gatfqvevpgsqhidsqkkai 86
                                                                                                                                                        92US-0945860
                                                                                                                       93WO-US08704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTB-CTP fusion protein.
                                                                                                                                                                                                                                                            WPI; 1994-118162/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
es 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
                                                                                                                                                                                                                                                                                  N-PSDB; AAQ45159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-APR-1999
                                                                                                                                                        16-SEP-1992;
                                                   WO9406465-A.
                                                                                      31-MAR-1994
                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW94082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                             Dale JB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expression of binding sub-unit protein of cholera toxin - using foreign promoter with no V cholera DNA between promoter and ribosome binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is produced by genetically fusing the leader sequence for E.coli heat-labile enterotoxin subunit (LTB) by its 3' SacI end to the 5' Ndel end of the chollera toxin subunit (CTB) via a syntheter linker. This allows the use of a strategically placed EcoRI site just upstream of the RBS on the LTB gene for the insertion of a strong tac promoter for the expression of CTB. The protein can be used as vaccines, cholera and receptor-blocking agents for prophylaxis.of cholera and E.coli diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B subunit; labile toxin; M protein; fusion protein; antigen; Group A streptococci; rheumatic fever; pharyngitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                    'label-cleavage to release mature CTB
                                                                                                                        to release mature CTB
25..28
/label=part of CTB leader sequence
                                                                                                                                                                                                                                                              /label=D = N in classical 569B CTB
                                                                                                                                                                                                                                                                                                 /label=D = N in classical 569 CTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 106; DB 11;
Pred. No. 2.3e-10;
; Mismatches 0;
                                                                                                                                                                                         abel=T = I in El Tor CTB
                                                                                                                                                                                                                           /label=G = S in El Tor CTB
                                                                                                                                                        abel-H - Y in El Tor CTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of LT-B-M24 hybrid molecule.
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                                                   /label=mature CTB
                                                                                                        25..26
⁄label≠cleavage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 21; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                      89EP-0850295
                                                                                                                                                                                                                                                                                                                                                                                                                                         88SE-0003291
                                                                                                                                                                                                                                                                                                                                                                                                                                                         89NO-0003702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sanches C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1990-149724/20.
P-PSDB; AAR04825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HOLM/) HOLMGREN J.
                                                                                                                                     Misc-difference 46
                                                                                                                                                                      Misc-difference 75
                                                                                                                                                                                                                                            Misc-difference 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 AA;
                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                             Misc-difference
                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                      11-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                       16-SEP-1988;
15-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holmgren J,
                                                                                                                                                                                                                                                                                                                                                                   16-MAY-1990
                                                                                                                                                                                                                                                                                                                                EP368819-A.
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 Peptide
                                    Protein
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AAR50227 RESULT

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Gaps

eg

Protein

Rock EP;

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A desired truncated gene is cut out from a plasmid in which the gD or gB gene (opt. lacking a transmembrane domain, full details not given for this sequence) of HSV-1 strain Miyama has been cloned. It can also be chemically synthesised.

An appropriated linker is added to it as needed, followed by construction of a fused gene in which an LTB gene is linked to the 3' end. The resulting fused protein gene is ligated downstream from a promoter in an expression vector.

The product is effecient for targetting to nasal mucosa tissues compared to unfused proteins. It can induce an immune response. The protein is useful as immunogen in vaccines for therapeutic and bacterial infections.
                                                                                                                                                                     Fused protein used to treat viral and pathogenic bacterial infections - contg. heat labile enterotoxin B sub-unit and herpes-simplex virus antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 106; DB 12;
100.0%; Pred. No. 8.6e-10;
ive 0; Mismatches 0;
                                                                            Yamamoto T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine; cholera; heat-labile E.coli toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of sub-unit B of cholera toxin.
                                                                                                                                                                                                                                               Disclosure; Page 13; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP50340 standard; protein; 103 AA.
                                                                              Mayumi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50..64
/note= "claimed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "claimed"
                                        (TAKE ) TAKEDA CHEMICAL IND KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GATFQVEVPGSQHIDSQKKAI 21
 89JP-0233728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84DE-3430894.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
45..64
                                                                            Hinuma S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                                               WPI; 1991-088294/13.
N-PSDB; AAQ11073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    405 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio cholera
 08-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-1984;
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                                                                            Fujisawa Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE3430894-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP50340;
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to breaking self-tolerance against self protein in a mammal that comprises administering a fusion protein for eliciting an immune response, the fusion protein comprising pentamers of Escherichia coll labile toxin subunit B (ITB) and carboxy terminal peptide (CTP) of human chorionic gonadotrophin (hCG). The fusion protein can also be used in a method of inducing antibody against protein in a mammal. The methods can be used to break self-tolerance and can produce antibodies to hCG. They can be used for prophylaxis and therapy, e.g. in the treatment of cancers or control of mammalian fertility. The method circumvents the chemical variability, complex preparation, side effects, and expense of other vaccines to break self tolerance that rely on passive immunisation, chemical conjugation with additional adjuvant, or lymphokine supplementation. The present sequence represents a LTB-CTP fusion
                                                                                                                                                                                                                                                                                                                                                           Breaking self-tolerance against self protein - using fusion proteins producing pentamers of Escherichia coli labile toxin subunit B and human chorionic gonadotrophin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSV-1 antigen/heat-labile enterotoxin B subunit fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herpes Simplex Virus-1; HSV-1; heat-labile enterotoxin;
subunit B; LTB; vaccine; nasal mucosa tissue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 106; DB 20;
100.0%; Pred. No. 3.1e-10;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSV-1 strain Miyama, Escherichia coli
134..149
/note= "CTP protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 4A-B; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR11272 standard; Protein; 405 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GATFOVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 gatfqvevpgsqhidsqkkai 86
                                                                                                                                97US-0944982
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97US-0944982
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Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                    WPI; 1999-152696/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 AA
                                                                                                                                                                                                                            (ROCK/) ROCK E P.
                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX06654.
                                                                                                                                07-JUN-1997;
                                                                                                                                                                     07-JUN-1995;
07-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-SEP-1990;
                                                        US5869057-A.
                                                                                             09-FEB-1999
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AAR11272

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Gaps

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Indels

Length 405;

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23-AUG-1994;
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31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                EP646599-A.
                                                                                                                                                                                                                                                                                             AAR72545;
                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    labile enterctoxin (Etx.) and its closely related homologue, cholers toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous GW-1 ganglioside receptors on host cells surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to peptide fragments of the Escherichia coli heat
                                                                                                 The inventors claim vaccines against cholera and heat-labile E.coli toxin contg. cholera toxin fragment coupled to carrier. The toxin is esp. the fragments defined in FT, above.
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the
                                                                                                                                                                                                                                                                                                                                                                                            Heat labile enterotoxin subunit B; EtxB;
beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation;
adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                     ő
                                                                                                                                                                                                                                                                                                                                                                         E. coli heat labile enterotoxin B-derived peptide, SEQ ID NO:5.
                                             Vaccines against cholera and heat-labile E. coli toxin - contg.
                                                                                                                                                                                Length 103;
                                                                                                                                                                                                     0; Indels
                                                                                                                                                                              Score 103; DB 6;
Pred. No. 5.6e-10;
L; Mismatches 0;
                                                        cholera toxin fragment coupled to carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 15; 62pp; English.
                                                                                                                                                                                                                                                                                                      AAY87463 standard; peptide; 21 AA.
                                                                                                                                                                                                                                               65
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                                                                                                                                                                              97.28;
95.28;
                                                                             Example; Fig 1; 24pp; German.
 Arnon R, Jacob CO;
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                                                                                                                                                                                                                                      1 GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycolipid receptor GM-1 -
                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                              Query Match 97.2
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Williams NA, Hirst TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYBR-) UNIV BRISTOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-256943/22.
                      WPI; 1985-069683/12.
                                                                                                                                               103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200014114-A1.
                                                                                                                                                                                                                                                                                                                                                  03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-2000
                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                            AAY87463;
Sela M,
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                                                                                                                                                                                                                                                                                            AAY87463
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beta-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 represent preferred peptides of the invention, AAY87460 being particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADP-ribosylating toxins, pertussis holotoxtin (PT), E. coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify stres which contribute to PT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella pertussis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      with
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hazes B, Klein MH, Loosmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP-ribosylating toxin; pertussis holotoxin; B-subunit; active site; E. coli heat labile toxin; verotoxin-1; Bordetella pertussis vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                        Score 101; DB 21;
Pred. No. 1.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP-ribosylating toxin (verotoxin-1 B-subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                        95.3%;
95.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0110947.
94US-0251121.
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Oomen R, Read RJ, Stein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 95.3
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYAL-) UNIV ALBERTA.
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                                                                                                                                                                                                                                                                                                                 21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other molecules
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55 21

GATFQVEVPGSQHIDSQKKAI

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AAW95226

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Involving analysis of the 3-dimensional form of the crystalline involving analysis of the 3-dimensional form of the crystalline holotoxin. The pertussis holotoxin modification process comprises: holotoxin. The pertussis holotoxin modification acid (aa) residue of the holotoxin for modification by analysing the 3-dimensional form of the crystalline holotoxin, in relation to known information of the protein structure and function; (2) effecting mutagenesis (by removing or replacing a nucleotide sequence encoding at least one (aa)) of a tox operon; and (3) expressing mutant tox box in a Bordetella organism to produce the modified holotoxin. This method is used for modifying pertussis holotoxin, by studying its 3-dimensional crystalline structure of the pertussis holotoxin, functional (aa) which affect bological properties of the pertussis holotoxin can be identified. This can be used to predict (aa) which affect bological properties of the pertussis holotoxin can be identified. This can be used to predict (aa) which affect bologicals properties of the pertussis holotoxin. The present sequence represents an ADP-ribosylating toxin and a production of the present sequence represents an ADP-ribosylating toxin a production of the present sequence represents an ADP-ribosylating toxin a production of the present sequence represents an ADP-ribosylating toxin a production of the present sequence represents an ADP-ribosylating toxin a production of the present sequence represents an ADP-ribosylating toxin a production of the present sequence represents an ADP-ribosylating toxin a production of the present sequence represents an ADP-ribosylating toxin a production of the present sequence represents an ADP-ribosylating toxin a production of the present sequence represents an ADP-ribosylating toxin a production of the present sequence represents an ADP-ribosylating toxin a production of the present sequence represents an ADP-ribosylating toxin a production of the present sequence represents and a production of the present sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP-ribosylating toxin; PT; crystalline pertussis holotoxin; ETA; DT; three-dimensional structure; LT; immunoprotective; infection.
                                                        Gaps
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       Length 93;
                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cockle SA, Loosmore S, Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New method for producing modified pertussis holotoxin
       Score 101; DB 16;
Pred. No. 1.1e-09;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli verotoxin-1 B-subunit.
                                                                                                                                                                                                                                                        AAY41816 standard; peptide; 93 AA.
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                                                                                                                   1 GATFQVEVPGSQHIDSQKKAI 21
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93US-0110947.
94US-0251121.
                            95.28;
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Query Match 95.3
Best Local Similarity 95.2
Matches 20; Conservative
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Oomen RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-579908/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                               08-DEC-1999
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Hazes B,
                                                                                                                                                                                                                                                                                                    AAY41816;
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The invention relates to methods of preparing a pertussis holotoxin (PT)
having a modified blological activity. One method comprises identifying
at least 1 site in a PT that interacts with a molecule that is capable of
comming a complex with the holotoxin and which molecule is an effector
molecule which is an adenine nucleotide and which site contributes to
controlly, cell binding or enzymatic activity of PT. The functional
interacting site(s) are identified by analysing the three dimensional
structure of crystalline PT, determined by X-ray crystallogaphy. The
identified interacting site(s) are modified to alter toxicity, cell
conting or enzyme activity of the PT. The methods can be used to alter a
blological activity such as toxicity, enzymatic activity, mitogenicity,
cell binding and adjuvanticity of the PT. The three-dimensional structure
of PT have functional and/or structural resemblance to other bacterial
toxins such as diphtheria toxin (DT), pseudomonas exotoxin A (ETA), the
heat-labile toxin of E. coli (LT) and verotoxin-1 (VT). The present
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                                                                                                                                              enzyme; ADP-ribosylation; toxin; crystalline; X-ray crystallography;
structural analysis; interacting site; mitogenicity; adjuvanticity;
                                                                                                                           Pertussis holotoxin; PT; modified; effector; toxicity; cell binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modifications to e.g. enzymatic activity, mitogenicity and cell binding of pertussin holotoxin - by identifying interaction sites of a molecule with crystalline toxin and modifying the identified site
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Klein MH, Loosmore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                             E. coli heat-labile toxin (LT) beta-subunit sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101; DB 20;
Pred. No. 1.1e-09;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                     B)
AAW95226 standard; peptide; 93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 مار، Cockle SA, Hazes
Read RJ, Stein PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 5; 40pp; English.
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94US-0251121
                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                   (UYAL-) UNIV ALBERTA.
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                                                                                                                                                                                                           Escherichia coli.
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                                                                                                                                                                            heat-labile; LT
                                                                                                                                                                                                                                                                                                                                                                                                                                     gD,
                                                                                                                                                                                                                                                                                                       22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1994;
                                                             16-MAR-1999
                                                                                                                                                                                                                                                                                                                                       22-AUG-1994;
                                                                                                                                                                                                                                        US5856122-A.
                                                                                                                                                                                                                                                                        05-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Armstrong
Oomen RP,
                               AAW95226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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Gaps

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Indels

Length 93;

95.3%; Score 101; DB 20; 95.2%; Pred. No. 1.1e-09; tive 0; Mismatches 1;

20; Conservative

Best Local Similarity

Query Match Matches

AAY68365;

AAY68365

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The present invention provides a method for producing a pertussis toxin (also designated lymphocytosis-promoting factor, histamine-sensitising factor and islet activating protein) with a modified biological activity, involving analysing the crystal structure of the protein to identify active sites which can then be modified. This may lead to an alteration in the toxicity, cell binding or enzyme activity of the toxin. This can be used in the production of immunoprotective analogues of pertussis toxin is the cause of whooping cough following infection
                                                                                                                                                                          Pertussis toxin; crystal structure; whooping cough; biological activity; lymphocytosis-promoting factor; histamine-sensitising factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modifying pertussis holotoxin to produce detoxified PT analogs, comprising analyzing crystalline structure of toxin, to identify sites of toxicity, cell binding or enzyme activity of PT and modifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oomen RP, Loosmore S, Klein MH, Armstrong GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exotoxin mucosal cell binding motif; nucleic acid delivery; nucleic acid affinity domain; heat-labile enterotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 101; DB 22;
Pred. No. 1.1e-09;
                                                                                                                     E coli verotoxin-1 B subunit SEQ ID NO: 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant exotoxin protein variant LTBpL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB73241 standard; Protein; 134 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 5; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0110947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0082514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0292968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GATFQVEVPGSQHIDSQKKAI
                                                       03-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                    islet-activating protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cockle SA,
Stein PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-122260/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.
                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93
                                                                                                                                                                                                                                                                                                                                                          US6168928-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    02-JAN-2001.
                                                                                                                                                                             Pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Read RJ,
Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB73241;
AAB66239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB73241
   NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Armstrong GD,
                                                                                                                                                                                                                                                                                                                                                Pertussis toxin; heat labile toxin; verotoxin; exotoxin A; holotoxin; diphtheria toxin; ADP-ribosylating toxin; mannose binding protein; infection; crystal structure; X-ray crystallography; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crystalline form of isolated pertussis holotoxin useful in studying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 101; DB 21;
Pred. No. 1.1e-09;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Loosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins which have functional resemblance
                                                                                                                                                                                                                                                                                            Heat labile toxin B subunit SEQ ID NO:26
                                                                                                            AAY68365 standard; Peptide; 93 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cockle SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 3; Fig 5; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0467976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93US-0110947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94US-0292968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                 17-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 95.3
Best Local Similarity 95.2
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stein PE,
Oomen RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-136703/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunogenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6018022-A.
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Read RJ, Hazes B,

(UXAL-)

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Gaps

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Indels

Unidentified.

AAB66239 standard; Protein; 93 AA.

AAB66239 ID AAB6 XX

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Sequence

Length 93;

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The present invention relates to recombinant exotoxin protein variants, affinity domain. The present sequence is one such protein variant. In the present invention the heat-lablie enterotoxin (LT) of Escherichia coli was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (bARE) family. The protein variants are useful for selectively delivering nucleic acid encodes an antigen to which the immune response when the nucleic acid encodes an antigen to which the immune response is desired, expression of a protein in a subject, by administering a composition comprising the protein variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid affinity domain. The present sequence is one such protein variant. In the present invention the heat-labile enterotoxin (LT) of Escherichia coll was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin
                                       Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding motif of an exotoxin and a nucleic acid affinity domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding motif of an exotoxin and a nucleic acid affinity domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exotoxin mucosal cell binding motif; nucleic acid delivery; nucleic acid affinity domain; heat-labile enterotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101; DB 22;
Pred. No. 1.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant exotoxin protein variant LTB-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB73243 standard; Protein; 155 AA.
                                                                                                                       Example 1; Fig 10; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.3%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-2000; 2000WO-US22715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0149294.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 getfqvevpgsqhidsqkkai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 95.3
Best Local Similarity 95.2
Matches 20, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 11; 57pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-211103/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AGRI-) AGRIVAX INC
                                                                                                                                                                                                                                                                                                                                                                                                           142 AA;
N-PSDB; AAF75713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAF75714.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB73243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid affinity domain. The present sequence is one such protein variant. In the present invention the heat-labile enterotoxin (LT) of Escherichia coli was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (bARE) family. The protein variants are useful for selectively delivering nucleic acid to mucosal cells, for inducing an immune response when the nucleic acid encodes an antigen to which the immune response is desired, for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein in a subject, by administering a composition
                                                                                                                                                                                                                                                                                                  Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding motif of an exotoxin and a nucleic acid affinity domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exotoxin mucosal cell binding motif; nucleic acid delivery; nucleic acid affinity domain; heat-labile enterotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 101; DB 22;
Pred. No. 1.7e-09;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant exotoxin protein variant LTBpLh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB73242 standard; Protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Fig 9; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising the protein variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.3%;
                                                                               18-AUG-2000; 2000WO-US22715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-AUG-2000; 2000WO-US22715.
                                                                                                                       99US-0149294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                          WPI; 2001-211103/21.
                                                                                                                                                              (AGRI-) AGRIVAX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-211103/21
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AGRI-) AGRIVAX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 AA;
WO200111960-A1
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AAB73242

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Indels

Length 142;

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(bARE) family. The protein variants are useful for selectively delivering nucleic acid to mucosal cells, for inducing an immune response when the nucleic acid encodes an antigen to which the immune response is desired, for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein in a subject, by administering a composition comprising the protein variant.
8888888
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155 AA; Sequence

Gaps ; Query Match 95.3%; Score 101; DB 22; Length 155; Best Local Similarity 95.2%; Pred. No. 2e-09; Matches 20; Conservative 0; Mismatches 1; Indels (

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Search completed: July 16, 2001, 16:35:41 Job time: 205 sec

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### Sequence 6, Application US/08952337

### APPLICANT: Lebens, Michael R.

### TITLE OF INVENTION: HYBRID MOLECULES BETWEEN HEAT-LABILE

### TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS

### TITLE OF INVENTION: BY SEA FOOTOXIN AND CHOLERA TOXIN B SUBUNITS

### CURRENT APPLICATION NUMBER: US/08/952,337

### CURRENT FILING DATE: 1998-01-05

### BARLIER PILING DATE: 1998-05-05

### BARLIER APPLICATION NUMBER: SE 9501682-0

### BARLIER APPLICATION NUMBER: SE 9501682-0
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US-08-961-810-133
US-08-352-902D-133
US-07-956-700B-94
US-08-485-607-94
US-08-485-607-94
US-08-602-359A-34
US-08-602-359A-34
US-09-025-580-36
S194375-6
US-08-714-070A-1
US-08-469-830-11
US-08-469-830-11
US-08-469-830-11
US-08-469-830-11
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US-08-469-830-11
US-08-469-8315
US-08-709-173-35
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Best Local Similarity
Matches 21; Conserv
               \begin{array}{c} \mathbf{u} \ \mathbf{
               TYPE: PRT
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Patent No. 5223510
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                                                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-84-526-2
US-08-913-047-2
US-09-314-597-2
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US-09-11-852-21
US-08-952-337-1
US-08-952-337-1
US-08-952-337-2
US-08-952-36-26
US-08-467-976-26
US-08-467-976-26
US-08-467-976-26
US-08-467-976-26
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Maximum Match 100%
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RESULT 5
US-09-013-047-2
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Patent No. 5932714
GENERAL INFORMATION:
APPLICANT: LOOSMOIRE, Sheena M.
APPLICANT: Zealey, Gavin R.
APPLICANT: Yacoob, Reza K.
APPLICANT: ALein, Michel H.
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Sim & MCBurney
STREET: 330 University Avenue, Suite 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 106; DB 3; Length 102; 100.0%; Pred. No. 2e-11;
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CUNTRY: Canada
ZIP: MAGG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION NUMBER: US/08/472,171
FILING DATE: 07-70N-1995
CLASSIFICATION NUMBER: US 08/393,334
ATLOND DATE: AFFEB-1995
ATTONEY/AGENT: NEPORMATION:
AND THE STATE OF THE COMPATION:
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100.0%; Pred. No. 2.1e-11;
tive 0; Mismatches 0;
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-507 MIS:vg
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
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TELEPHONE: 416-595-1155
TELEFAX: 416-595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 GATFQVEVPGSQHIDSQKKAI 64
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2
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LENGTH: 103 amino acids
TYPE: amino acid
                                                                                                                                                                                                       ; ORGANISM: Escherichia coli
US-08-952-337-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 21; Conservi
                                                                                                                           LENGTH: 102
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                                                                                                                                                                     TYPE: PRT
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                                                                                     APPLICANT: Taccob, Reza K
APPLICANT: Zealey, Gavin R
APPLICANT: Zealey, Gavin R
TITLE OF INVENTION: EXPRESSION OF GENE PRODUCTS FROM
TITLE OF INVENTION: GENETICALLY MANIPULATED STRAINS OF BORDETELLA
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: SIM & MCBurney
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                                                                                                                                                                                                                                                                                                                                                                               SUFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/08/894,526 FILING DATE: US/08/894,526 CLASSIFICATION: 435 ATTORNEX/AGENT TWOMAREY.
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Pred. No. 2.1e-11;
; Mismatches 0;
                                                                                                                                                                                                                                        ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
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STREET: 330 University Avenue, 6th Floor
CITY: Toronto
                                                                                                                                                                                                                                                                                                       STATE: Ontario
COUNTY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DC
Sequence 2, Application US/08894526 Patent No. 5942418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stewart, Michael I
REGISTRATION UNDRER: 24,973
REFERENCE/DOCKET UNDRER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELERAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09013047
Patent No. 5998168
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Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: LOOSMOCE, Sheena M.
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
                                                                   APPLICANT: Loosmore, Sheena M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-894-526-2
                                               GENERAL INFORMATION:
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Indels

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APPLICANT: Charles J. Arntzen, Hugh S. Mason, and Tariq A. Haq
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCES: ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 MCKinney, Suite 5100
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,852
                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 106; DB 4;
100.0%; Pred. No. 2.1e-11;
Live 0; Mismatches 0;
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Pred. No. 2.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 24-CT-1995
APPLICATION NUMBER: .08/817,906
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: FOX, DAYIG L.
REGISTRATION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: P01590US1
                  NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038-964
TELECOMMUNICATION INFORMATION:
TELEPRONE: 416-595-1155
TELERX: 416-595-1163
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/09191852; Patent No. 6194560; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 713-651-5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
100.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-374-597-2
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Best Local Similarity
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Best Local Similarity
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ZIP: 77010
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TOPOLOGY:
US-09-191-852-21
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US-09-191-852-21
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                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 106; DB 2; ilarity 100.0%; Pred. No. 2.1e-11; Conservative 0; Mismatches 0;
                                                                                                                                                                  CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNDERER:
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,334
FILING DATE: 23-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-507 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEFHONE: 416-595-1155
TELEFAX: 416-595-115
TELEFAX: 416-595-115
TELEFAX: 416-595-115
TELEFAX: 416-595-115
TELEFAX: 416-595-115
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STREET: 330 University Avenue, 6th Floor
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/374,597
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
PLUBLICATION NUMBER: 08/393,334
FILING DATE: FEBRUARY 23, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LOOSMOTE, Sheena M.
APPLICANT: Yacob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Lein, Michel H.
TITLE OF INVENTION: Expression O
TITLE OF INVENTION: Genetically
NUBBE OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09374597 Patent No. 6140082 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 103 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: protein US-09-013-047-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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COUNTRY: Canada
ZIP: MSG 1R7
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Best Local Similarity
Matches 21; Conserv
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APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REPERENCE: 3846/00758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1996-05-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER PILING DATE: 1996-05-05
EARLIER PILING DATE: 1996-05-05
EARLIER FILING DATE: 1995-05-05
SOFTWARE: FASTER OF TOWNER: PSOFT DATE: PSOFT
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STREET: 3100 No. 5993820west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 123;
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Pred. No. 2.6e-11;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                          Score 106; DB 3;
Pred. No. 2.6e-11;
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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APPLICANT: BAGDASARIAN, Michael
APPLICANT: IRELAND, James
TITLE OF INVENTION: CHIMERIC LTB VACCINES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER FILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 123
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100.0%; Prf
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Patent No. 6019973
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Best Local Similarity 100.0%; P
Matches 21; Conservative 0;
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Eschcerichia coli
US-08-952-337-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                     ; ORGANISM: Vibrio cholerae US-08-952-337-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-08-952-337-2
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US-08-747-410-2
                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                           Sequence 21, Application PC/TUS9513376
GENERAL INFORMATION:
APPLICANT: The Texas A&M University System
APPLICANT: 310 Wisenbaker.
APPLICANT: College Station, Texas 77843-3369
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 103;
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APPLICANT: Holmgren, Jan
APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES ATOXIN B SUBUNITS
FILE REFERENCE: 3846/0D758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PACETING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACETIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 106; DB 5;
100.0%; Pred. No. 2.1e-11;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/328,716
FILING DATE: 24-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jones, John W.
REGISTRATION NUMBER: 31,380
REGISTRATION NUMBER: 36170/3P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08952337
Patent No. 6019973
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TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
                                                                                                  45 GATFQVEVPGSQHIDSQKKAI 65
                                                               1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GATFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 103 amino acids TYPE: amino acid
      21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Best Local Similarity
Matches 21; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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         Matches
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Gaps
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Patent No. 5965385

GENERAL INFORMATION:
APPLICANT: STEIN, Penelope E.
APPLICANT: OOMEN, Raymond P.
APPLICANT: OOMEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICANTON OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BR PC COMPATIBLE
APPLICATION NUMBER: US/08/467,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 95.3%; Score 101; DB 2; Best Local Similarity 95.2%; Pred. No. 1.4e-10; Matches 20; Conservative 0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
                              FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/251,121
FILING DATE: 31-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael 1.
RECISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-388
TELEPAN: (416) 595-1155
TELEPAN: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-UN-1995
FILING DATE: 22-AUG-1994
PRIOR APPLICATION NUMBER: US 08/292,968
FILING DATE: 31-MAY-1994
PRIOR APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
FILING DATE: 31-AAG-1994
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY:
US-08-292-968-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: STEIN, Penelope E.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COCKLE, Stephen A.
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: HAZES, Bart
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES:
ADDRESSEE: Sim & MCBURDEY
STREET: Sulte 701, 330 University Avenue
CITY: TOCORC
STAFE: Ontario
COUNTRY: Canada
ZIP: MSG IR7
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPAING
COMPUTER: STAFE : PLOSP/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 106; DB 2;
100.0%; Pred. No. 2.6e-11;
Live 0; Mismatches 0;
                                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M
REGISTRATION NUMBER: 33,924
REFRENCE/DOCKET NUMBER: 11526.1-US-01
TELEPHONE: 612/371-5268
TELEPHONE: 612/371-5268
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM VESTEON 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,410
FILING DATE: 12.NOV-1996
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
ATTONNOM
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/292,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26, Application US/08292968 Patent No. 5856122 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66 GATFQVEVPGSQHIDSQKKAI 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     internal
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Length 93;

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1; Indels
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STATE: Ontario

STATE: Ontario

COUNTRY: Canada

ZIP: MSG 1R7

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.25

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,976

FILING APPLE : 06-UUN-1995

FILING APPLICATION: A35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
                                                                                                                                                                                           Score 101; DB 2;
Pred. No. 1.4e-10;
0; Mismatches 1;
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Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Suite 701, 330 University Avenue CITY: Toronto STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-453 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26, Application US/08467976
Patent No. 6018022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T: READ, Randy J.
T: STEIN, Penelope E.
T: COCKLE, Stephen A.
T: OOMEN, Raymond P.
T: LOOSMORE, Sheena
T: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                         1 GATFQVEVPGSQHIDSQKKAI 21
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95.2%;
                                                                                                                                                                                           Query Match 95.3%;
Best Local Similarity 95.2%;
Matches 20; Conservative
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26
                                            single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
            TYPE: amino acid
STRANDEDNESS: sis
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Best Local Similarity
                                                                        linear
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-08-467-536-26
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APPLICANT: STEIN, Penelope E.
APPLICANT: CCCKLE, Stephen A.
APPLICANT: COCKLE, Stephen A.
APPLICANT: LOOSWORE, Sheena
APPLICANT: LOOSWORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: HAZES, Bart
ITILE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:

COMPUTER: IDAN C COMPATION OF SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,536

FILING DATE: 06-JUN-1995

FILING DATE: 06-JUN-1995

FILING DATE: 06-JUN-1995

TOWNS OF THE CONTROL OF THE CON
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 101; DB 2;
Pred. No. 1.4e-10;
0; Mismatches 1.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-454 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
TELEPAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acid
STRANDENBESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION NUMBER: US 08/251,121
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY AGENT INFORMATION:
NAME: STEWART, MICHAEl I.
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-455 MIS:V9
TELECOMMNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26, Application US/08467536 Patent No. 5977304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35 GETFQVEVPGSQHIDSQKKAI 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                         95.3%;
95.2%;
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 95.3
Best Local Similarity 95.2
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                ; TOPOLOGY:
US-08-467-974-26
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Length 93;

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Gaps
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Pred. No. 7.5e-10;
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GENERAL INFORMATION:
APPLICANT: Burnette, Neal W.
APPLICANT: Railow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/829,026A
FILING DATE: 18-AUG-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk,
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,045C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
STREET: Soom 411, Building 005, BARC-W
CITY: Beltsville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: US/08/449,045C
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APPLICATION NUMBER: US 07/694,733
FILING DATE: 02-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08449045C Patent No. 5770203
                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.4
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0106
TELECOMUNICATION INFORMATION:
TELEPHONE: 301-504-5676
TELEFAX: 301-504-5060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49 GETFQVEVPGSQHIDSQKKAI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95.3%;
95.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 371 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-829-026A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 24
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-449-045C-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 18
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APPLICANT: Meinersmann, Richard J.
APPLICANT: Khoury, Christian A.
TITLE OF INVENTION: Campylobacter Jejuni Flagellin-Escherichia Coli LT-B Fusion P
      Gaps
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COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,514
FILING DATE:
CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION NUMBER: US 08/292,968
FILING APPLICATION NUMBER: US 08/292,968
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             MODIFICATION OF PERTUSSIS TOXIN
      ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.3%; Score 101; DB 4; 95.2%; Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
    Mismatches
                                                                                                                                                                    US-09-082-514-26
; Sequence 26, Application US/09082514
; Patent No. 6168928
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08829026A
Patent No. 5837825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1153
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                    APPLICANT: STEIN, Penelope E. APPLICANT: STEIN, Penelope E. APPLICANT: COCKLE, Stephen A. APPLICANT: COMEN, RAYMOND P. APPLICANT: KLEIN, Michel H. APPLICANT: HAZES, BAIT TILE OF INVENTION: MODIFICATION NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35 GETFQVEVPGSQHIDSQKKAI 55
                                                                 35 GETFQVEVPGSQHIDSQKKAI 55
                                            1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6th Floor, 330 United STREET: 6th Floor, STATE: Ontario COUNTRY: Canada ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GATFQVEVPGSQHIDSQKKAI 21
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Best Local Similarity 95.2
Matches 20; Conservative
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20;
Matches
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Gaps

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APPLICANT: Burton, Frank H.; Sutcliffe, Gregor
TITLE OF INVENTION: CHOLERA TOXIN GENE REGULATED BY GROWTH
HORMONE PROMOTER
                                                                                                                                                                                                                                                                                                                                                                                                                                             88.7%; Score 94; DB 6; Length 124; 90.5%; Pred. No. 3.3e-09; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN TITLE OF INVENTION: KINASES NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS: ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IDEM Compatible
OMPUTER: IDEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION UMBER:
RILING DATE:
RILING DATE:
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                                                                                                                                                                 NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,852
FILING DATE: 18-MAY-1990 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08878989
Patent No. 5885803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bandman, Olga
Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 GAIFQVEVPSSQHIDSQKKAI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guegler, Karl G.
Lal, Preeti
Goli, Surya K.
Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Corley, Neil C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 88.7
Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                             5223610
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                                                                                                                                                                                                                                                                                                                         LENGTH: 124
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                            SEQ ID NO:3:
                                             :Patent No.
            5223610-3
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US-08-435-605A-12
Sequence 12, Application US/08435605A
Factor No. 5874287
GENERAL INFORMATION:
APPLICANT: Burnette, W. Neal
APPLICANT: Burnette, W. Neal
APPLICANT: RASIOW, HARVEY R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STATE: California
COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: INP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
CORPUTER: US-MATE OS-MAY-1995
FILING DATE:
FIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                88.7%; Score 94; DB 1; Length 124; 90.5%; Pred. No. 3.3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
FILING DATE: 06-JUL-1994
MINDER MAZZA, RICHARD J.
REGISTRATION NUMBER: 27 657
REFERENCE/DOCKET NUMBER: A-190
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: MAZZA, RICHARD J.
REGISTRATION NUMBER: 27.657
REFRERUCE/DOCKET NUMBER: A-196
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 GAIFQVEVPSSQHIDSQKKAI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GATFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 90.59
Matches 19; Conservative
                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-449-045C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-435-605A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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IMMEDIATE SOURCE: LIBRARY: TBLYNOT01

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GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotosh,
TITLE OF INVENTION: TANG-15: An Extracellular Serine Protease Overexpressed in
TITLE OF INVENTION: Breast and Ovarian Carcinomas
TITLE OF INVENTION: Breast und Ovarian Carcinomas
TITLE OF INVENTION: Breast und Ovarian Carcinomas
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 2
LENGTH: 855
                                                                                                                                                                                                                                                                                                                                                   CTHER INFORMATION: Amino acid sequence of TADG-15 encoded by nucleotides OTHER INFORMATION: 23 to 2589 of Sequence 1; Patent No. 5972616 US-09-027-337-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08709784

Patent No. 6048701

CENERAL INFORMATION:
APPLICANT: The Johns Hopkins University
ITILE OF INVENTION: Antibody Detection of Mismatch Repair
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-FOOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/709,784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 2;
Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Banner & Allegretti, Ltd. 1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1107.57434
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FILING DATE:
ATTORNEY, AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE, POCKET NUMBER: 1107
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                        ; Sequence 2, Application US/09027337B
; Patent No. 5972616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
   269 GOSINVHIPNSQKVDSQKAA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
6, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TFQVEVPGSQHI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                       RESULT 23
US-09-027-337-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-709-784-2
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                                                                     DB 2; Length 448; 0.55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 448
                                                                                                          8; Indels
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                                                                                                                                                                                                                                                           SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48.1%; Score 51; DB 4 50.0%; Pred. No. 0.55;
                                                                   48.1%; Score 51; DB 50.0%; Pred. No. 0.55 tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0321 US
TELEPHONE: 415-855-0555
TELEFANX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                             269 GQSINVHTPNSQKVDSQKAA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TELYNOTO1
CLONE: 40194
                                                                                                                                         1 GATFQVEVPGSQHIDSQKKA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GATFQVEVPGSQHIDSQKKA 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                      Best Local Similarity 50.09
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.03
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
; CLONE: 40194
US-08-878-989-2
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                                                                                                                                                                                                                              RESULT 22
US-09-272-796-2
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US-09-272-796-2
                                                                     Query Match
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Gaps

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Sequence 23, Application US/08209521

Sequence 23, Application US/08209521

Sequence 23, Application US/08209521

Sequence 23, Application

Sequence 24, Sept. S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC Compatible
COMPUTER: BLACHIN Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/209,521
FILIG DATE: 08-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Van Rysselberghe, Pierre C.
REGISTRATION NUMBER: 33,557
REFERENCE/DOCKET NUMBER: 0450
TELEPHONE: (503) 224-6655
TELEPHONE: (503) 295-6679
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENDOTH: 862 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 85;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 38.2%; Score 40.5; I Best Local Similarity 75.0%; Pred. No. 86; Matches 9; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.2%; Score 40.5; 75.0%; Pred. No. 85
LENGTH: 856 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                               MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
CRANISM: Homo sapiens
US-08-709-784-2
                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 38.2
Best Local Similarity 75.0
Matches 9; Conservative
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TOPOLOGY: linear
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MOLECULE TYPE: protein
US-08-209-521-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 GSQ-HIDSQKKA 20
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US-08-209-521-23
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1; Gaps

0; Indels

10 GSQ-HIDSQKKA 20

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| 528 GSQEHVDSQEKA 539
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Search completed: July 16, 2001, 16:36:18 Job time: 207 sec

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version 4.5
- 2000 Compugen Ltd.
GenCore
Copyright (c) 1993
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 protein search, using sw model OM protein Run on:

July 16, 2001, 16:37:01; Search time 34.9 Seconds (without alignments) 45.836 Million cell updates/sec

1 GATFQVEVPGSQHIDSQKKAI 21 US-09-786-648-4 106 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

pir1:* pir2:* pir3:* pir4:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

	Description	heat-labile entero	cholera enterotoxi	RAD23 protein homo	hypothetical prote		Q,	hypothetical prote			Ω	queuine tRNA-ribos	kinesin heavy chai	chorismate synthas	hypothetical prote	chitinase (EC 3.2.	stress-activated p	inner membrane pro	probable carnitine	4-aminobutyrate tr	alpha-dextrin endo	conserved hypothet	ubiquitin / riboso	ubiquitin / riboso	ubiquitin 18 - sli	ubiquitin (clone l	polyubiquitin 5 (c	polyubiquitin 5 (c		yaan protein - Bac
SUMMARIES	OI	OLECB	XVVCB	T04150	T19866	C86400	D81715	C96580	A86457	S76110	н69231	T46898	T49189	S17246	F83962	JG0178	JC5694	G81692	T49574	JC4022	S11823	F81109	UQDOR	UQDOR7	D34080	B27806	C34080	B34080	A27806	866056
	Length DB	124 1	124 1	392 2	374 2	574 2	374 2	91 2	255 2	1742 2	365 2	399 2	439 2	376 1	216 2	•		787 2			1090 2	91 2	128 1	154 1	228 2	229 2	380 2	380 2	381 2	386 1
æ	Query Match I	95.3	94.3	45.3	43.4	43.4	42.0	41.5	41.5	41.5		40.6	40.6	40.1	39.6	39.6	39.6	39.6	39.6	39.5	39.5	38.7	38.7	38.7	38.7	38.7	38.7	38.7	38.7	38.7
	Score	101	100	48	46	46	44.5	44	44	44	43	43	43	42.5	42	42	42	42	42	41.5	41.5	41	41	41	41	41	41	41	41	41
	Result No.	-	7	3	7	5	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	50	21	22	23	24	25	56	27	28	29

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polyubiquitin 7 (c hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote hypothetical prote	protein F20B17.2 [	hypothetical prote	gibberellin 20-oxi	hypothetical prote	thiosulfate sulfur	thiosulfate sulfur	hypothetical prote	hypothetical prote	RNA binding protei
A34080 T01770	T20566 S47598	669903	T32894 T34767	C96827	T24938	T01751	T04861	T52658	T01034	T16225	T16655	T39064
0.0	~ ~	(1)	N N	~	~	~	7	7	7	~	~	7
532 550	2911 862	105	227	260	355	367	368	378	379	461	603	655
38.7	38.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7
41	41	40	4 4 0 4	40	40	40	40	40	40	40	40	40
30 31	33.2 33.2	34	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1				
QLECB				
heat-labil	heat-labile enterotoxin c	chain	B precursor	-

C;Species: Escherichia coli C;Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change 18-Jun-1999 C;Accession: A01820; B26946; I41194; I41287; I67644; A61475

Escherichia coli

R;Dallas, W.S.; Falkow, S. Nature 288, 499-501, 1980
A;Title: Amino acid sequence homology between cholera toxin and Escherichia coli heat A;Reference number: A01820; MUID:81074965
A;Accession: A01820

A;Molecule type: mRNA A;Residues: 1-124 <0bb. K;Yanamoto, T.; Gojobori, T.; Yokota, T. J. Bacteriol. 169, 1352-1357, 1987 A;Tatle: Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichi A;Reference number: A26946; MUID:87137303 A;Reference: B26946 A; Wolecule type: DNA A; Residues: 1-27, KE, 29-63, KK', 65-124 < YAM> A; Cross-references: EMBL.M15363; NID:9148335; PIDN:AAA24792.1; PID:9148336 A; Cross-references: EMBL.M5363; NID:9148335; PIDN:AAA24792.1; PID:9148336 R; Leong, J.; Vinal, A.C.; Dallas, W.S. Infect. Immun. 48, 73-77, 1985 A; Title: Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons A; Reference number: 141194; MUID:85156481

A; Status: preliminary A:Accession: 141194

A; Molecule type: DNA A; Residues: 1-5, Fr',7-17, C',19-24,'S',26-27,'E',29-33,'H',35-63,'K',65-66,'A',68-122 A; Cross-references: GB:M17874; NID:g145830; PIDN:AAA98064.1; PID:g145831 A; Experimental source: plasmid ENT-R PCG86 R; Ibrahimi, I.; Gentz, R. J. Biol. Chem. 262, 10189-10194, 1987 A; Title: A functional interaction between the signal peptide and the translation appa

A; Reference number: 141287; MUID:87280041 A; Accession: 141287 ticulum

A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA A; Residues: 1-22 <RE2>

A;Cross-references: GB:M17101; NID:g146375; PIDN:AAA23973.1; PID:g146376
A;Cross-references: GB:M17101; NID:g146375; PIDN:AAA23973.1; PID:g146376
K;Inoue, T.; Tsuji, T.; Koto, M.; Imamura, S.; Miyama, A.
FEMS Microbiol. Lett. 108, 157-161, 1993
A;Title: Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic A;Reference number: 153542; MUID:93252225

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-1,'C', 19,'Y',21-24,'S',26-27,'E',29-63,'K',65-66,'A',68-122,'E',124 <R A;Residues: 1-1,'C', 19,'Y',21-24,'S',26-27,'E',29-63,'K',65-66,'A',68-182',E',124 <R A;Cross-references: GB:S60731; NID:9408994; PIDN:AACG0441.1; PID:9408996 R;Tsuji, T.; Lida, T.; Honda, T.; Miwatani, T.; Nagahama, M.; Sakurai, J.; Wada, K.; Microb. Pathog. 2, 381-390, 1987

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A,Accession: A21910
A,Accession: A21910
A,Molecule type: protein
A,Residues: 22-38,'H',40-42,'N',44-67,'T',69-90,'N',92-124 <TAK>
A,Experimental source: biotype Inaba 569B
A,Note: Asn-65 was partially deaminated to Asp
C;Comment: The authors translated the codon TCA for residue 33 as Tyr.
C;Gometics: A,Gene: VC1456
A,Map position: I
C;Complex: the cholera enterotoxin molecule contains three kinds of chains; an alpha ciate noncovalently with the subunit B, an aggregate of five beta chains
C;Function: involved in binding of the toxin to cell membranes
C;Function: A,Description: toxin beta chain
C;Keywords: enterotoxin; toxin
                                          Alcoechim. Biophys. Acta 1090, 139-141, 1991
A.Title: Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classic A.Recession: S17665; MUID: 91355224
A.Recession: S17665; MUID: 9135524
A.Recession: S17666
A.Molecule type: DNA
A.Residues: 1-38, "4', 40-67, "T', 69-124 < DA2>
A.Cross-references: EMBL: X58785; NID: 94888; PIDN: CAA41591.1; PID: 948890
R:Ma, O.J.; Liu, C.X.; Xiong, L.S.; Yu, X.O.
Sci. Sin. B Chem. Biol. Agric. Med. Barth Sci. 34, 274-280, 1991
A.Title: B subunit of cholera toxin produced in Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A;Residues: 22-38, H',40-67, T',69, E',71,'QS',74-75,'VE',78-86,'Q',88-99,'Q',101-103
R;Takao, T.; Watanabe, H.; Shimonishi, Y.
ET. J. Biochem. 146, 503-508, 1985
A;Title: Facile identification of protein sequences by mass spectrometry.
A;Reference number: A21910; MUID:85126976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 22-38, 'H', 40-41 < MAQ>
R; Residues: 22-38, 'J-1; Swartz, D.J.; Pearson, G.D.N.; Harford, N.; Groyne, F.; de Wilde, Nature 306, 551-557, 1983
A; Reference number: A93320; MUID: 84068199
A; Recession: A05130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 22-38, "H', 40-42, "N', 44-67, "T', 69, "E', 71-90, "N', 92-124 <LAI>
A; Residues: 22-38, "H', 40-42, "N', 44-67, "T', 69, "E', 71-90, "N', 92-124 <LAI>
A; Note: the difference at residue 70 may be due to deamidation during preparation
B; Nakashima, Y.; Naplorkowski, P.; Schafer, D.E.; Konigsberg, W.H.
FEBS Lett. 68, 275-278, 1976
A; Title: Primary structure of the B subunit of cholera enterotoxin.
A; Reference number: A38034; MUID:77026365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Determination of the primary structure of cholera toxin B subunit. A;Reference number: A38033; MUID:78005536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-32, 'S', 34-74,'S', 76-124 < MEK>
A; Residues: 1-32, 'S', 34-74,'S', 76-124 < MEK>
A; Cross-references: GB:X00171; NID:948347; PIDN:CAA24996.1; PID:9758351
A; Cross-references: GB:X00171; NID:948347; PIDN:CAA24996.1; PID:9758351
B; Kurosky, A.; Markel, D.E.; Peterson, J.W.
J. Biol. Chem. 252, 7257-7264, 1977
A; Title: Covalent structure of the beta chain of cholera enterotoxin.
A; Reference number: A1819; MUID:78005537
A; Accession: A01819
A; Molecule type: protein
A; Residues: 22-38,'H', 40-42,'N', 44-67,'T', 69-90,'N', 92-124 < KUR>
B; Lai. C.Y.
                          de Wolf, M.; Dierick, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.3%;
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A; Title: A unique amino acid sequence of the B subunit of a heat-labile enterotoxin isol A; Reference number: A61475; MUID:89180953
A; Reference number: A61475
A; Mocession: A61475
A; Residues: 22-24, S; Z6-27, E', 29-63, K', 65-66, A', 68-95, A', 97-122, E', 124 <TSU>A; Residues: 22-24, S', Z6-27, E', 29-63, K', 65-66, A', 68-95, A', 97-122, E', 124 <TSU>A; Residues: 22-24, S', Z6-27, E', 29-63, K', 65-66, A', 68-95, A', 97-122, E', 124 <TSU>A; Residues: 22-24, S', Z6-27, E', 29-63, K', 65-66, A', 68-95, A', 97-122, E', 124 <TSU>A; Residues: B; Residues: Residues: B; Residues: B; Residues: B; Residues: B; Residues: B; Residues: B; Residues: Residues:
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95.2%; Pred. No. 1.6e-09;
1ive 0; Mismatches 1;
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Length 574;

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Dypothetical protein F1511.6 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: One F2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: C96580 C;Accession: C96580 M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Chin, C.W.; Chung, M.K.; Conn, L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Reference number: A86141; MUID:21016719
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A;Cross-references: GB:AE002300; GB:AE002160; NID:g7190365; PIDN:AAF39192.1; PID:g719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-574 <STO>
A;Cross-references: GB:AE005172; NID:g5668763; PIDN:AAD45990.1; GSPDB:GN00141
C;Genetics:
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Pred. No. 12;
2; Mismatches
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48.0%;
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A; Status: preliminary
A; Molecule type: DNA
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hypothetical protein AAD45890.1 [imported] - Arabidopsis thaliana
hypothetical protein AAD45890.1 [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C86400
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
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A)CLOSS-references: EMBL:281482; PIDN:CAB03954.2; GSPDB:GN00028; CESP:C40H5.3
A)Experimental source: clone C40H5
C)Genetics:
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                                                                                                                                                                                                                                                                                                             RAD23 protein homolog - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein C40H5.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T19866
R;White, S.
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A,Map position: X
A;Introns: 44/2; 95/1; 178/1; 234/3; 348/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C40H5.3
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RySchultz, T.F.; Quatrano, R.S.
Rystile: Characterization and expression of a rice RAD23 gene.
RyReference number: Z08695; MUID:97369378
A;Reference number: Z08695; MUID:97369378
A;Reference number: T04150
A;Reference number: Z08695; MID:97369378
A;Reference number: Z08695
A;Re
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42.1%; Pred. No. 7.7;
Live 2; Mismatches
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A;Molecule type: DNA
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A;Reference number: 219189
A;Accession: T19866
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42.9%; Pred. No. 3
               66 GAIFQVEVPGSQHIDSQKKAI 86
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Matches 9; Conservative
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Best Local Similarity
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A; Pathway: queuosine biosynthesis; tRNA modification
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87;
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A;Cross-references: EMBL:L33777; PIDN:AAA27704.1
A;Accession: T46899
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                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Complex: monomer [validated; MUID:95394847]
                                                                                                                                               Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.68;
36.88;
                                                                                                                                               41.5%;
38.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 AIFLVKIPGGELVDANRSA 67
                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                               Query Match
Best Local Similarity
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Function:
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A.Reference number: S74322; MUID:97061201
A.Accession: S76110
A.Status: nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-1742 <KAN>
A.Residues: 1-1743 <KAN>
A.Residues: 1-1743 <KAN>
A.Residues: 1-1743 <KANA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Theologis, A.T. Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.Yitle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.Accession: A86457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein - Synechocystis sp. (strain PCC 6803)

C;Species: Synechocystis sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C;Accession: S76110

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;

O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda

DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
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                                                                                                                                         A;Cross-references: GB:AE005173; NID:g4587538; PIDN:AAD25769.1; GSPDB:GN00141
C;Genetics:
A;Gene: F1511.6
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein AAG21605.1 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Aate: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 R;Rrheologis, A.: Ecker. I P. P. 1.
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                                                                                                                                                                                                                                                                                                                             DB 2;
3.6;
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                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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4; Mismatches
                                                                                                                                                                                                                                                                                                                             Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44;
A; Reference number: A86141; MUID:21016719
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                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 GKTFNLEVKGSEIIQQVKNMI 78
                                                                                                                                                                                                                                                                                                                             41.5%;
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Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-255 <STO>
                                                                                  A; Molecule type: DNA
A; Residues: 1-91 <STO>
                                                         A; Status: preliminary
                           A; Accession: C96580
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C; Species: Methanobacterium thermoautotrophicum
C; Species: Methanobacterium thermoautotrophicum
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C; Sancta, D.S.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Oliv, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, J. Bacteriol. 179, 7135-7155, 1997
A; Tile. S.; Church, G. M.; Dandels, C. J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
A; Reference number: A69000; MUID:98037514
A; Reference number: A69000; MUID:98037514
A; Accession: H69231
A; Molecule type: DNA
A; Residues: 1-365 <MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:AE000872; GB:AE000666; NID:g2622082; PIDN:AAB85482.1; PID:g262 A;Experimental source: strain Delta H C;Genetics: A;Genetics: A;Gene: WTH985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rikeuter, K.; Ricner, R.
J. Bacteriol. 177, 5284-5288, 1995
A;Title: Sequence analysis and overexpression of the Zymomonas mobilis tgt gene encod
A;Reference number: 224129; MUID:95394847
A;Reference number: 224129; MUID:95394847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Description: (EC 2.4.2.29) [validated; MUID:95394847]; catalyzes the exchange of gu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sensory transduction histidine kinase - Methanobacterium thermoautotrophicum (strain
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Genetics:
A;Start codon: GTG
                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                     Length 1742;
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A;Molecule type: DNA
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Length 376;

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C; Species: Glycine max (soybean)
C; Species: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 21-Jul-2000
C; Accession: JG0178
R; Watanabe, A.; Nong, V.H.; Zhang, D.; Arahira, M.; Yeboah, N.A.; Udaka, K.; Fukazawa Biosci. Biotechnol. Biochem. 63, 251-256, 1999
A; Title: Molecular cloning and ethylene-inducible expression of Chibl chitinase from A; Reference number: JG0178; MUID:99208985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06221.1; GSPDB:G
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                            C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C;Accession: F83962
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A;Accession: F83962
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                                                                                                                                                                                                                                                                                                                                                               hypothetical protein BH2502 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stress-activated protein kinase (EC 2.7.-.-) JNKb - common carp
     F;347-363/Domain: transmembrane #status predicted <TMM>
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Pred. No. 28;
3; Mismatches
                                                                           Score 42.5; DE
Pred. No. 29;
2; Mismatches
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Best Local Similarity 38.1%;
Matches 8; Conservative
                                                                             40.1%;
62.5%;
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258 GSGFQGVSVPGSKHND 273
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                                                                                                                                Conservative
                                                                                                                                                                                1 GATFQ-VEVPGSQHID 15
                                                                           Query Match
Best Local Similarity
Matches 10; Conserv
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Matches 7; Conserv
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A; Residues: 1-216 <STO>
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A; Residues: 1-299 <WAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chorismate synthase (EC 4.6.1.4) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G2501; protein YGL148w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: S17246; S64162
R;Jones, D.G.L.; Reusser, U.; Braus, G.H.
Mol. Microbiol. 5, 2143-2122, 1991
A;Title: Molecular cloning, characterization and analysis of the regulation of the ARO2
A;Recession: S17246; MuID:92114793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-376 <VOL>
A; Residues: 1-376 <VOL>
A; Cross-references: EMBL: 272670; NID:91322731; PIDN:CAA96860.1; PID:91322732; GSPDB:GNOC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, submitted to the Protein Sequence Database, April 2000 A;Reference number: 225018
C;Superfamily: queuine tRNA-ribosyltransferase
C;Keywords: glycosyltransferase; magnesium; metalloprotein; pentosyltransferase; tRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Nap position: 3
A;Introns: 39/3; 74/1; 97/3; 138/3; 147/2; 193/3; 200/2; 273/3; 304/2; 341/3; 401/3
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N;Alternate names: protein MAA21.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun.2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49189
                                                                                                                                                           Gaps
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A; Residues: 1-376 <100N
A; Residues: 1-376 <10N
A; Cross-references: EMBL:X60190; NID:93386; PIDN:CAA42745.1; PID:93387
R; Volckaert, G.; Voet, M.; Verhasselt, P.; Defoor, E.
submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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A; Cross-references: EMBL:AL163818; GSPDB:GN00061; ATSP:MAA21.110
A; Experimental source: cultivar Columbia; BAC clone MAA21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 439,
                                                                                                        Length 399
                                                                                                                                                           Indels
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C;Superfamily: chorismate synthase
C;Keywords: phosphorus-oxygen lyase; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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26;
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Pred. No. 29;
                                                                                                                                                        Mismatches
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A;Cross-references: SGD:S0003116; MIPS:YGL148w
                                                                                                     Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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                                                                                                   40.6%;
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                                                                                                                                                        Conservative
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A; Accession: S64162
                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 8; Conserv
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Gaps

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Indels

Length 216;

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Gaps

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10; Indels

2; Length 299

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A; Experimental source: BAC clone B208; strain OR74A
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J. Bacteriol. 171, 3673-3679, 1989
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55.6%;
                                                                                                                                                                                                                               39.68;
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Best Local Similarity 55.6
Matches 10; Conservative
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A; Residues: 1-1090 <KOR>
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Best Local Similarity
Matches 8; Conserv
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                                                                 A;Gene: NCSP:B208.220
A;Map position: 6
A;Introns: 138/1
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A;Molecule type: DNA
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                                       C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                Cross-references: DDBJ:AB001744; NID:g2467307; PIDN:BAA22598.1; PID:d1023466; PID:g246; Comment: This enzyme is a mitogen-activated protein kinase, and plays a role in egg ma Superfamily; unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C. Accession: G81692

R. Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Accession: G81692

R. Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Godson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000

A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.

A; Reference number: A81500; MUID:20150255

A; Accession: G81692

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-787 < CTETY

A; Cross-references: GB: AE002321; GB: AE002160; NID: G7190560; PIDN: AAF39364.1; PID: G719056

A; Genetics:
A; Genetics: A; Gwinn, Migg (MoPn)
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N;Alternate names: protein B208.220
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49574
S;Chulte, U.; Algn, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, Submitted to the Protein Sequence Database, May 2000
A;Reference number: 22502
A;Accession: T49574
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-864 <SCH>
N; Alternate names: stress-activated protein kinase b (5; Species: Cyprinus carpio (common carp) (c) Species: Oyprinus carpio (common carp) (c) Accession: UC5694 (c) Aritle: Structure and expression of carp mitogen-activated protein kinases homologous A; Reference number: UC5693; MUID: 97456373 (c) Aritle: Structure and expression of carp mitogen-activated protein kinases homologous A; Reference number: UC5694 (c) A; Residue: nucleic acid sequence not shown A; Molecule type: mRNA A; Residues: 1-427 cHAS.> A; Residues: 1-427 cHAS.> A; Residues: 1-427 cHAS.> A; Residues: 1-427 cHAS.> A; Cross-references: DDBJ-AB001744; NID: 92467307; PIDN: BAA22598.1; PID: d1023466; PID: 92467; C; Comment: This enzyme is a mitogen-activated protein kinase, and plays a role in egg management.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inner membrane protein, probable TC0522 [imported] - Chlamydia muridarum (strain Nigg) C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
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Pred. No. 41;
0; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Superfamily: unassigues co. C; Keywords: phosphotransferase F:24-278/Domain: protein kinase homology <KIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 39.6%;
Best Local Similarity 61.5%;
Matches 8; Conservative
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Matches 8; Conserv
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G81692
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R;Osei, Y.D.; Churchich, J.E. Gene 155, 185-187, 1995.
A;Tile: Screening and sequence determination of a cDNA encoding the human brain 4-am A;Reference number: JC4022; MUID:95237607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A, Experimental source: brain
C, Comment: This enzyme catalyzes the conversion of 4-aminobutyrate, the inhibitory ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Title: Klebsiella pneumoniae puls gene encodes an outer membrane lipoprotein requir
A:Reference number: A32880; MUID:89291709
A:Accession: A32880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAlternate names: pullulanase
C;Species: Klebsiella pneumoniae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: S11823; A32880
R;Kornacker, M.G.; Pugsley, A.P.
Mol. Microbiol, 4, 73-85, 1990
A;Title: Molecular characterization of pulA and its product, pullulanase, a secreted
A;Reference number: S11823; MUID:90205629
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                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 18-Jun-1999
                                                                Gaps
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A;Residues: 1-500 <OSE>
A;Cross-references: GB:L32961; NID:g602704; PIDN:AAA74449.1; PID:g602705
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Length 864;
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                                                                                                                                                                                                                                                                                                                                    4-aminobutyrate transaminase (EC 2.6.1.19) - human
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Score 42; DB;
Pred. No. 88;
3; Mismatches
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Pred. No. 59; 4; Mismatches
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A;Map postition: 19q13-19q13
C;Superfamily: 4-aminobutyrate transaminase
C;Keywords: aminotransferase
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C; Superfamily: ubiquitin/ribosomal protein CEP52; ribosomal protein CEP52 homology; u C; Superfamily: blading; protein biosynthesis; protein degradation; ribosome; zinc fi F; 1-76/Product: ubiquitin #status predicted <UBI>F; 1-76/Product: ubiquitin homology <UBH>F; 77-128/Product: ribosomal protein CEP52 #status predicted <RIB>F; 77-128/Pomain: ribosomal protein CEP52 #status predicted <RIB>F; 77-128/Pomain: ribosomal protein CEP52 homology <CPH>F; 77-128/Pomain: ribosomal protein CEP52 homology <CPH
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A.Residues: 1-154 <0HNS)
A.Cross-references: GB:M23750; GB:J02858; NID:g167940; PIDN:AAA33264.1; PID:g167941
A.Cross-references: GB:M23750; GB:J02858; NID:g167940; PIDN:AAA33264.1; PID:g167941
C.Superfamily: ubiquitin / rat ribosomal protein S27a; ribosome
C.Keywords: protein biosynthesis; protein degradation; ribosome
F):1-76/Product: ubiquitin %textus predicted <MATI>
F):1-76/Domain: ubiquitin protein S27a #status predicted <MATI>
F):77-154/Product: ribosomal protein S27a #status predicted <MATI>
F):102-152/Domain: ribosomal protein S27a homology <RIB>
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Biochemistry 28, 5226-5231, 1989
A;Title: Molecular organization of developmentally regulated Dictyostellum discoideum
A;Reference number: A34080; MUID:89352609
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Biochemistry 28, 5226-5231, 1989
A;Title: Molecular organization of developmentally regulated Dictyostelium discoideum
A;Reference number: A34080; MUID:89352609
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C.Species: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
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C;Date: 30-Mar-1990 #șequence_revision 30-Mar-1990 #text_change 23-Feb-1997
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C; Superfamily: polyubiquitin 3; ubiquitin homology
C; Keywords: duplication; nucleus; polyprotein; protein degradation
F; 776,Domain: ubiquitin homology <UBH2>
F; 777-152/Domain: ubiquitin homology <UBH2>
F; 153-228/Domain: ubiquitin homology <UBH3>
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Pred. No.
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Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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R;Ohmachi, T.; Giord
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A.; Molecule type: DNA
A.; Residues: 1-91 < TET>
A.; Cross-references: GB:AE002469; GB:AE002098; NID:g722646; PIDN:AAF41600.1; PID:g722645
A.; Experimental source: serogroup B, strain MC58
B.; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
B.; Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
B.; Parkhill, J.; Achtman, M.; Leather, S.; Moule, S.; Mungall, K.; Ouail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A.; Reference 404, 502-506, 2000
A.; Reference number: A81775; MUD:2022556
A.; Accession: F81907
A.; Status: preliminary
A.; Molecule type: DNA
A.; Residues: 1-91 < PAR>
A.; Cross-references: GB:AL157959; NID:g7379742; PIDN:CAB84626.1; PID:g738004
A.; Experimental source: serogroup A, strain 22491
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A.; Genetics:
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R; Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Ti, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755
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A;Title: Complete cDNA sequence of a Dictyostellum ubiquitin with a carboxy-terminal A;Reference number: S00357; MUID:88152253
A;Molecule type: mRNA
A;References: S00357
A;Molecule type: mRNA
A;Residues: 1-128 < MUID:
A;Re
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C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
C;Accession: S00357; A258663
E;Mueller-Taubenberger, A.; Westphal, M.; Jaeger, E.; Noegel, A.; Gerisch, G
FEBS Lett. 229, 273-278, 1988
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N;Alternate names: ubiquitin fusion protein
C;Species: Dictvostellum Ainceles
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                                      A;Cross-references: GB:M29097; NID:g342046; PIDN:AAA61976.1; PID:g643577 C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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llarity 38.5%; Pred. No. 1.4e+02;
Conservative 4; Mismatches 7;
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Sequence: 1 GATFQVEVPGSQHIDSQKKAI 2
Scoring table: BLOSUM62
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Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters:

93435

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Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	P13811 escherichia	P32890 escherichia	P01556 vibrio chol	014896 homo sapien		sacch	homo	homod	klebs		Q09217 caenorhabdi	P37535 bacillus su		P20163 caenorhabdi	Q10005 caenorhabdi	Q92347 schizosacch		P16342 murine coro		P20220 sulfolobus		Q9hkt0 thermoplasm		P51882 rattus norv	P27420 caenorhabdi	P53699 candida alb	P14882 rattus norv	P36598 schizosacch	P31870 hepatitis b	P29982 murine coro	90	P25276 pseudomonas	P13128 listeria mo
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or send an email to license@isb-sib.ch).
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"Crystal structure of the B subunit of escherichia coli heat-labile enterotoxin carrying peptides with anti-herpes simplex virus type 1
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Leong J., Vinal A.C., Dallas W.S.;
"Nucleotide sequence comparison between heat-labile toxin B-subunit
cistrons from Escherichia coli of human and porcine origin.";
Infect. Immun. 48:73-77(1985).
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                                                                                                                  -1- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED BY THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
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                                                                                         Chem. 274:8764-8769(1999)
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MEDLINE-81074965; PubMed-7003397;
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EMBL; J01646; AAB02982.1; -.
EMBL; S60731; AAC60441.1; -.
EMBL; X83966; CAA58800.1; -.
PDB; LLTR; 23-MAR-99.
InterPro; IPR001835; -.
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Best Local Similarity 100.
Matches 21; Conservative
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Nature 288:499-501(1980)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Crystal structure of a cholera toxin-related heat-labile enterotoxin
SEQUENCE FROM N.A.
STRAIN=ISOLATE PCG66;
MEDLINE=81137303, Pubmed=3546273;
Yamamoto T., Gojobori T., Yokota T.;
"Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichia coli and Vibrio cholerae 01.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MDDLINES_2138966; PubMed=2034287;
Sixma T.K., Pronk S.E., Kalk K.H., Wartna E.S., van Zanten B.A.M., Witholt B., Hol W.G.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sixma T.K., van Zanten B.A.M., Dauter Z., Hol W.G.J.;
Refined structure of Escherichia coli heat-labile enterotoxin, a
close relative of cholera toxin.";
J. Mol. Biol. 230:890-918 (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domenighin M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R.; Domenighin M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R.; Identification of errors among database sequence entries and comparison of correct amino acid sequences for the heat-labile enterotoxins of Escherichia coli and Vibrio cholerae."; Mol. Microbiol. 15:1165-1167(1995).

-!- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED BY THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-!- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-22 FROM N.A.
MEDLINE-87280041; PubMed-3301830;
Ibrahimi I., Gentz R.;
"A functional interaction between the signal peptide and the translation apparatus is detected by the use of a single point mutation which blocks translocation across mammalian endoplasmic
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MEDLINE-93240541; PubMed-8478941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol. Chem. 262:10189-10194(1987).
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EMBL; M15363; AAA24792.1; -.
EMBL; M17101; AAA23973.1; -.
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Nature 351:371-377(1991).
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PDB; 1LT6; 03-DEC-97.
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PDB; 1LT4; 16-JUN-97
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PIR; B26946; QLECEB.
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us-09-786-648-4.rsp

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EMBL;
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EMBL;
PIR; A
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STRAIN=EL TOR 2125;
MEDLINE=84068199; PubMed=6646234;
Mekalanos J.J., Swartz D.J., Pearson G.D.N., Harford N., Groyne F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amamoto K., Do V.G.R.F., Xu M., Iida T., Miwatani T., Albert M.J.,
                                                                                                                                                                                                                                                                                Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                             MEDLINE-84061784; PubMed-6315707;
Lockman H., Kaper J.B.;
"Nucleotide sequence analysis of the A2 and B subunits of Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                "Cholera toxin genes: nucleotide sequence, deletion analysis and vaccine development.";
Nature 306:551-557(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=4260B / SEROTYPE 0139;
MEDLINE-94237453; Pubmed=8181723;
Lebens M., Holmgren J.;
"Structure and arrangement of the cholera toxin genes in Vibrio
                                                                                                                                                ;
0
                                                                                                                                Length 124;
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=EL TOR 2125;
Dams E., de Wolf M., Dierick W.;
Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                          14133 MW; 6DB7DE58395EA70D CRC64;
                                                                                                                       95.3%; Score 101; DB 1; Le
95.2%; Pred. No. 1.3e-09;
utematches 1;
                                                                                                                                                                                                                 CHTB_VIBCH STANDARD; PRT; 124 AA. P01556; Q9JQ02; 21-JUL-1986 (Rel. 01, Created) 13-AGC-1987 (Rel. 05, Last sequence update) 10-CT-2000 (Rel. 40, Last annotation update) CHOLERA ENTEROTOXIN, BETA CHAIN PRECURSOR. CTXB OR TOXB OR VC1456.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMS Microbiol. Lett. 117:197-202(1994).
                                                                                                                                                                                                                                                                                                                                    cholerae enterotoxin.";
J. Biol. Chem. 258:13722-13726(1983)
                                                                                                                                                                      66 GETFQVEVPGSQHIDSQKKAI 86
                                                                                                                                                              1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-1854 / Ol39-BENGAL;
                                                                                                                                               20; Conservative
107
30
32
32
43
51
51
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77
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Best Local Similarity
Matches 20; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                        Vibrio cholerae
                                                                                                                                                                                                                                                                                       NCBI_TaxID=666;
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CHTB_VIBCH
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=EL TOR N16961 / SEROTYPE O1;
MEDIJNE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Glil S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING TO CELL MEMBRANES.
-!- SUBUNIT: CONTAINS 3 KINDS OF CHAINS. AN ALPHA AND A GAMMA CHAIN
-(FROM THE SAME PRECURSOR MOLECULE), LINKED BY AN INTERCHAIN
DISULFIDE BOND, ASSOCIATE NONCOVALENTY WITH AN AGGREGATE OF 4 TO
6 BETA CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Determination of the primary structure of cholera toxin B subunit."; J. Biol. Chem. 252:7249-7256(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Crystal structure of cholera toxin B-pentamer bound to receptor GM1 pentasaccharide.";
Protein Sci. 3:166-175(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=OGAWA 41 / CLASSICAL BIOTYPE;
MEDLINE=9737625; PubMed=9223653;
Merritt E.A., Sarfaty S., Jobling M.G., Chang T., Holmes R.K.,
Hirst T.R., Hol W.G.J.;
"Structural studies of receptor binding by cholera toxin mutants.";
"Structural studies of receptor binding by cholera toxin mutants.";
Protein Sci. 6.1516-1528 (1997).
-i. FUNCTION: THE BETA CHAIN AGGREGATE (B SUBUNIT) IS INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE-94272319; PubMed-8003954;
Merritt E.A., Sarfaty S., van den Akker F., L'Hoir C., Martial J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-95387394; PubMed-7658472; Zhang R.G., Westbrook M.L., Westbrook E.M., Scott D.L., Otwinowski Maulik P.K., Reed R.A., Shipley G.G.; "The 2.4 A crystal structure of cholera toxin B subunit pentamer: choleragenoid.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 22-124.
MEDLINE-78005537; PubMed=903363;
Kurosky A., Markel D.E., Peterson J.W.;
"Covalent structure of the beta chain of cholera enterotoxin.";
J. Biol. Chem. 252:7257-7264(1977).
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MEDLINE-78005536; Pubmed-903362;
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[11]
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A01819; XVVCB.
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EMBL; D30053; BAA06291.1;
EMBL; X58786; CAA41593.1;
EMBL; X76390; CAA53973.1;
EMBL; X76391; CAA53976.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 406:477-483(2000).
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                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
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MEDLINE-96256303; PubMed-8654383;
Romler C., Reuter K., Suck D., Ficner R.;
"Crystal structure of tRNA-guanine transglycosylase: RNA modification by base exchange.";
By base exchange.";
EMBO J. 15:2850-2857(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE FROM N.A. STRAIN-ATCC 31821 / ZM4 / CP4;
STRAIN-ATCC 31821 / ZM4 / CP4;
MEDLINE-92406015; Pubmed-1526462;
Shark K.B., Conway T.;
"Cloning and molecular characterization of the DNA ligase gene (lig)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS).
Graedler U., Gerber H.D., Goodeneough-Lashua D.M., Garcia G.A.G.,
Finen R., Feuter K., Stubbs M.T., Klebe G.;
"A new target for shigellosis: rational design and crystallographic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-95394847; PubMed-765516;
Reuter K.K.H., Ficner R.;
Sequence analysis and overexpression of the zymomonas mobilis tgt gene encoding tRNA-guanine transglycosylase: purification and biochemical characterization of the enzyme.";
J. Bacteriol. 177:5284-5288(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonas group;
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928720; 060247;
01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
0-MAY-2000 (Rel. 39, Last Ennotation update)
UDGINE TRNA-REDSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRNA-GUANINE INSERTION ENZYME).
                                                                                                                                                                                                                                                                                                                                                                                                                           1; Length 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., SEQUENCE OF 1-6, AND CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                     PROBLES, FOUNDER, AND TRANSCRIPTION FOR TRANSCRIPTION FEGULATION, BIND 9 111 TRYPHOPHAN PENTAD REPEAT. SENDENCE 467 AA; 53129 WW; 7E28F5E0F5BA4053 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                         41.5%; Score 44; DB
41.2%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches
-! - SIMILARITY: BELONGS TO THE IRF FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from Zymomonas mobilis.";
FEMS Microbiol. Lett. 75:19-26(1992).
                                                                                                                                                                                        EMBL; AF027292; AAB84111.1; -. EEMBL; AAL02299; CAA18545.1; -. HSSP; P23906; 1IRG. INTERPRO; IPR001346; -.
                                                                                                                                                                                                                                                              Pfam; PF00005; IRF; 1.
PRINTS; PR00267; INTFRNREGFCT.
PROSITE; PS00601; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 QVKFPGPEHITNEKQKL 289
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=542;
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  STAN PARKARAN STAN
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_raxID=9606;
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                                                                                                                                                                                                                                                                                                         CHOLERA ENTEROTOXIN, BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.3%; Score 100; DB 1; Length 124, 95.2%; Pred. No. 1.9e-09; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grossman A., Mittrucker H.W., Antonio L., Ozato K., Mak
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grafham D.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9AA393E3EA8E3EBF CRC64;
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AND
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERFERON REGULATORY FACTOR 6 (IRF-6).
                                                                                                                                                                                                                                                                     Membrane; Enterotoxin; Signal; 3D-structure.
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                                                                                                                                                                                                          InterPro; IPR001835; -. Pfam; PF01376; Enterotoxin_B; 1.PRINTS; PR00772; ENTEROTOXINB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
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            PIR: S14624; S14624.
PDB: 3CHB: 03-DEC-97.
PDB: 1CHP: 08-MAR-96.
PDB: 1CHQ: 08-MAR-96.
PDB: 1FGB: 23-DEC-96.
PDB: 1FGB: 23-DEC-96.
PDB: 1XTC: 01-AUG-97.
PDB: 1CTI: 15-OCT-97.
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014896;
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Query Match

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MEDLINE-92114793; PubMed-1837329;
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Q9Y5Y6;
                                                                                                                                   cerevisiae
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ST14_HUMAN
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         ID DATE OF STREET OF STREE
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                                                                                                                                                                                                                                                                                                                                                                     -!- SUBUNIT: MONOMER.
-!- SIMILARITY: BELONGS TO THE QUEUINE TRNA-RIBOSYLTRANSFERASE FAMILY.
-!- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY DUE
studies of inhibitors of tRNA-guanine transglycosylase.";
Submitted (MAR-2000) to the PDB data bank.

-!- FUNCTION: EXCHANGES THE GUANINE RESIDUE WITH 7-AMINOMETHYL-7-
DEAZAGUANINE IN TRNAS WITH GU(N) AWINICODONS (TRNA-ASP, -ASN, -HIS
AND -TXR). AFTER THIS EXCHANGE, A CYCLOPENTENDIOL MOIETY IS
ATTACHED TO THE 7-AMINOMETHYL GROUP OF 7-DEAZAGUANINE, RESULTING
IN THE HYPERMODIFIED NUCLEOSIDE QUEUGSINE (Q) (7-((4,5-CIS-
DINYDROXY-2-CYCLOPENTEN-1-Y1)AMINO)METHYL)-7-DEAZAGUANOSINE).
-!- CATALYTIC ACTIVITY: TRNA GUANINE + QUEUINE = TRNA QUEUINE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CHORISMATE SYNTHASE (EC 4.6.1.4) (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                              -1- COFACTOR: BINDS AND REQUIRES ZINC FOR ACTIVITY. ALSO REQUIRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Queuosine biosynthesis; Transferase; Glycosyltransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tRNA processing; Zinc; Magnesium; 3D-structure.
INIT_MET 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L33777; AAA27704.1; ALT_INIT.
EMBL; L33777; AAA27705.1; ALT_INIT.
EMBL; Z11910; -; NOT_ANNOTATED_CDS.
PDB; 1PUD; 07-JUL-97.
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PDB; 1WKE; 07-JUL-97.
PDB; 1ENU; 19-APR-00.
InterPro; 1PR002616; -
Pfam; PF01702; TGT; 1.
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Best Local Similarity
Matches 8; Conserv
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P28777;
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ACT_SITE
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                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=97197983; PubMed=9046099;

MEDLINE=97197983; PubMed=9046099;

MEDLINE=97197983; PubMed=9046099;

MEDLINE=97197983; PubMed=9046099;

NOTICE TO THE SEQUENCE OF A DEALTY UNCLOADULE 22.8 kb segment on the left arm chromosome VII from Saccharomyces cerevisiae reveals ARO2, RPL9A,

TIP1, MRFH genes and six new open reading frames.";

Yeast 13:177-182(1997);

LICATALYTIC ACTIVITY: 5-0-(1-CARBOXYVINYL)-3-PHOSPHOSHIKIMATE =

CHORISMATE + ORTHOPHOSPHATE.

CI-COPACTOR: REDUCED FLANIN.

CI-COPACTOR: REDUCED FLANIN.

CI-COPACTOR: REDUCED RANININ THE BIOSYNTHESIS OF CHORISMATE WITHIN THE BIOSYNTHESIS OF AROMATIC ANINO ACIDS (THE SHIKIMATE PATHWAY).

CI-SUBULIT: HOMOTETRAMER (BY SIMILARITY).

CI-SUBULITY: BY AMINO ACID STRRYMION.

CI-SIMILARITY: BELONGS TO THE CHORISMATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
SUPRESSOR OF TUMORIGENICITY 14 (EC 3.4.21.-) (MATRIPTASE) (MEMBRANE-
TYPE SERINE PROTEASE 1) (MT-SP1).
Jones D.G.L., Reusser U., Braus G.H.; Molecular cloning, characterization and analysis of the regulation of the ARO2 gene, encoding chorismate synthase, of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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MEDLINE-99303581; PubMed=10373424;
Lin C.Y., Anders J., Johnson M., Sang Q.A., Dickson R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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Pfam; PF01264; Chorismate_synt; 1.
PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.
PROSITE; PS00789; CHORISMATE_SYNTHASE_2; 1.
PROSITE; PS00789; CHORISMATE_SYNTHASE_3; 1.
Lyase; Aromatic amino acid blosynthesis.
SEQUENCE 376 AA; .40838 MW; AF3AF65605B91E8E CRC64;
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                                                                                                                                                      Mol. Microbiol. 5:2143-2152(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X60190; CAA42745.1; -. EMBL; X99960; CAA68214.1; -. EMBL; Z72670; CAA96860.1; -. PIR; S17246; S17246.
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Matches 10; Conservative
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                                                                                                                                     TISSUE-MILK:

X Pubmed-1073425;
A Lin C.Y. Anders J., Johnson M., Dickson R.B.;
Lun C.Y. Anders J., Johnson M., Dickson R.B.;
Lun C.Y. Anders J., Johnson M., Dickson R.B.;
Luntification and characterization of a complex containing matriptase
T and a Kunitz-type serine protease inhibitor from human milk.";
J. Balol. Chem. 274:18237-18242(1999).
L. J. BALOL Chem. 274:18237-18242(1999).
C -!- FUNCTION: DEGRADES EXTRACELLULAR MATRIX. PROPOSED TO PLAY A ROLE
IN BREAST CANCER INVASION MAD METASTASIS. EXHIBITS TRYPSIN-LIKE
C OR LYS AS THE P1 SITE
C -!- SUBLEMENTY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.
C -!- SIMILARITY: CONTAINS 2 CUB DOMAINS.
C -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
TRYPSIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
"Molecular cloning of cDNA for matriptase, a matrix-degrading serine
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                                                        Takeuchi T., Shuman M.A., Craik C.S.;
"Reverse blochemistry: Use of macromolecular protease inhibitors the dissect complex blological processes and identify a membrane-type serine protease in epithelial cancer and normal tissue.";
Proc. Natl. Acad. Sci. U.S.A. 96:11054-11061(1999).
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CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
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PRIMIS; PRO0722; CHYMOTRYPSIN.
PROSITE; PSO0134; TRYPSIN_HIS; 1.
PROSITE; PSO1136; TRYPSIN_SER; 1.
PROSITE; PSO1180; CUB; 2.
PROSITE; PSO1299; LDLRA_1; 2.
PROSITE; PSO0689; LDLRA_2; 4.
Signal-anchor; Glycoprotein; Hydrolase; Serine protease;
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LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
CATALYTIC.
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           protease with trypsin-like activity.";
J. Biol. Chem. 274:18231-18236(1999).
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Interpro; IPR001314; -.
Interpro; IPR002172; -.
Pfam; PF00057; 1dl_recept_a; 4.
Pfam; PF00089; trypsin; 1.
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                                              SEQUENCE FROM N.A.
                                                                                                                              CHARACTERIZATION.
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CARBOHYD
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                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medina-Kauwe L.K., Tobin A.J., De Meirleir L., Jaeken J., Jakobs C.,
Nyhan W.L., Gibson K.M.;
"4-aminobutyrate aminotransferase (GABA-transaminase) deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- DISEASE: DEFECTS IN ABAT ARE A CAUSE OF GABA-AT DEFICIENCY WHOSE PHENOTYPE INCLUDES PSYCHOMOTOR RETARDATION, HYPOTONIA, HYPERREFLEXIA, LETHARGY, REFRACTORY SEIZURES, AND EEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEMINIDERYDE + L-GLUTANATE.
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: MONOMER (PROBABLE).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- TISSUE SPECIFICITY: LIVER > PANCREAS > BRAIN > KIDNEY > HEART >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           de Biase D., Barra D., Simmaco M., John R.A., Bossa F.; "Primary structure and tissue distribution of human 4-aminobutyrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a cDNA encoding the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
N-LINKED (GLCNAC. ..) (POTENTIAL) 26143132C01F99C9 CRC64;
                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
4-AMINOBUTYRATE AMINOTRANSFERASE, MITOCHONDRIAL PRECURSOR
(EC 2.6.1.19) (GAMMA-MINO-N-BUTYRATE TRANSAMINASE) (GABA
TRANSAMINASE) (GABA AMINOTRANSFERASE) (GABA-AT).
                                                                                                                      Length 855
                                                                                                                                                                                     Indels
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                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            500 AA
                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  brain 4-aminobutyrate aminotransferase.
                                                                                                                         Score 42;
                                                                                                                                                         Pred. No.
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Eur. J. Biochem. 227:476-480(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-99336116; PubMed-10407778;
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MEDLINE=95237607; PubMed=7721088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
                               94769 MW;
                                                                                                                      39.6%;
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                                                                                                                                                                                     6; Conservative
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367 TWNIEVPNNQHV 378
                                                                                                                                                                                                                                             3 TFQVEVPGSQHI 14
                               855 AA;
                                                                                                                      Query Match
Best Local Similarity
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CARBOHYD
SEQUENCE
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UBIQUITIN
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ACT_SITE
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LD UBIO_D
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MEDLINES #603461; PubMed=3902792;
Chapon C., Ratbaud O.;
"Structure of two divergent promoters.located in front of the gene encoding pullulanase in Klebsiella pneumoniae and positively regulated by the malf product.";
J. Bacteriol. 164:639-645(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1988 (Rel. 07, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
01-OCT-2000 (Rel. 40, Ec. 3.2.1.41) (ALPHA-DEXTRIN ENDO-1,6-ALPHA-GLUCOSIDASE) (PULLULANA 6-GLUCANOHYDROLASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kornacker M.G., Pugsley A.P.; "Molecular characterization of pulA and its product, pullulanase, secreted enzyme of Klabsiella pneumoniae UNF5023."; Mol. Microbiol. 4:73-85(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Klebsiella pneumoniae.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                  4-AMINOBUTYRATE AMINOTRANSFERASE.
PYRIDOXAL PHOSPHATE.
R -> K (IN GABA-AT DEFICIENCY; 25%
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D'Enfert C., Pugsley A.P.;
"Klebsiella pneumoniae pulS gene encodes an outer membrane lipoprotein required for pullulanase secretion.";
J. Bacteriol. 171:3673-3679(1989).
                      InterPro; IPR000954; -. 3; 1. Pfam; PF00202; aminotran_3; 1. PROSITE; PS00600; AA_TRANSFER_CLASS_3; 1. Transferase; Aminotransferase; Pyridoxal phosphate; Mucotransmitter degradation; Mitochondrion; Transit peptide; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 500
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                                                                                                                                                                                                        ACTIVITY)
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V -> L (IN REF. 2
E -> G (IN REF. 2
C -> G (IN REF. 2
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S -> A (IN REF. 2
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D -> H / TM ==
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EMBL; L32961; AAA74449.1; -. MIM; 137150; -.
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17 TYRLLVPGSRHI-SQAAA 33
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Best Local Similarity 55.6
Matches 10; Conservative
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P07206;
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BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                         -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO KNOWN AS THE ALPHA-AMYLASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                         SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A LIPID ANCHOR (PROBABLE).
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(1-6)-ALPHA-GLUCOSIDIC LINKAGES IN PULLULAN AND STARCH FORM MALTOTRIOSE.
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T -> N (IN REF. 2).
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EMBL; M12503; AAA52087.2; -.
EMBL; M25097; AAA61976.1; -.
PIR; A25025, A25025.
PIR; A32880; A3280.
PIR; S11823; S11823.
PIR; S11823; S11823.
PFO0128; alpha-amylase; 1.
Pfam; PFO0128; alpha-amylase; 1.
Pfam; PFO0128; APROKAR_LIPOPROTEIN; 1.
Hydrolase; Glycosldase; Membrane; Lipoprotein; Signal.
SIGNAL
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBL_TaxID=44689;
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Last annotation update)
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FEBS Lett. 229:273-278(1988).
[2]
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Matches 10; Conservative
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                                                    SUBUNIT: HOMOTRIMER.
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                                                                                                                                                                                                                            Westphal M., Mueller-Taubenberg A., Noegel A., Gerisch G.;
"Transcript regulation and carboxyterminal extension of ubiquitin in
Dictyostellum discoldeum":
FEBS Lett. 209:92-96(1986).
-I- FUNCTION: INVOLUED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF
CELLULAR PROFEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE,
REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
                                                                                                               MEDLINE-87257921; PubMed-3037345;
Giorda R., Enhis H.L.;
"Structure of developmentally regulated Dictyostelium discoideum
ubiquitin genes.";
                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
MISCELLANEOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN
PRECURSOR WITH EXACT HEAD TO TAIL REPEATS. SOME UBIQUITIN GENES
CONTAIN A SINGLE COPY OF UBIQUITIN FUSED TO A RIBOSOMAL PROTEIN.
           MEDLINE-89352609; PubMed-2548604; Mimachi T., Giorda R., Shaw D.R., Ennis H.L.; Molecular organization of developmentally regulated Dictyostellum discoideum ubiquitin cDNAs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MULTIUBLQUITIN ADDUCTS. CONJUGATION TO ACCEPTOR PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K -> N (IN SOME CLONES REPEATS).
6427383968EA8A84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NECESSARY FOR BRANCHED-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X07210; CAA30183.1; ALT_TERM. EMBL; M19666; AAA33261.1; ALT_TERM. EMBL; M19491; AAA33261.1; ALT_TERM. EMBL; M23748; AAA33261.1; ALT_TERM. EMBL; M23749; AAA33262.1; ALT_TERM. EMBL; M23750; AAA33262.1; ALT_TERM. EMBL; M23750; AAA33264.1; ALT_TERM. EMBL; M23751; AAA33265.1; ALT_TERM. EMBL; M23753; AAA33266.1; ALT_TERM. EMBL; M23754; AAA33266.1; ALT_TERM. EMBL; M23754; AAA33266.1; ALT_TERM. EMBL; M23754; AAA33268.1; ALT_TERM. EMBL; X04702; CAA28408.1; ALT_TERM.
                                                                                                                                                          ubiquitin genes.";
Mol. Cell. Biol. 7:2097-2103(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00299; UBIQUITIN_1; 1.
PROSITE; PS50053; UBIQUITIN_2; 1.
                                                                    Biochemistry 28:5226-5231(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nuclear protein; Polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MΨ.
                                                                                                                                                                                                   SEQUENCE OF 13-76 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00348; UBIQUITIN.
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PIR; A27806; A27806.
PIR; B34080; A34080.
PIR; B34080; A34080.
PIR; C34080; B34080.
PIR; C34080; D34080.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P02248; 1AAR.
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 SEQUENCE FROM N.A.
                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 AA;
                                                                                                                                                                                                                                                                                                                                BIOGENESIS
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                                                                                                                                                                                                                   STRAIN-AX2
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Score 41; DB 1; Length 76;

38.7%;

Query Match

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  Gaps
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ogasawara N., Nakai S., Yoshikawa H.; Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin."; DNA Res. 1:1-14(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kirsten J.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: SOME, TO YEAST YDL087C AND S.POMBE SPCC16All.13.
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01-OCT-1994 (Rel. 30, Last sequence update)
01-EEB-1996 (Rel. 33, Last annotation update)
HYPOTHETICAL 43.8 KDA PROTEIN IN XPAC-ABRB INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 313;
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  Indels
                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 37.0 KDA PROTEIN B0495.8 IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36977 MW; 000D2327621BFED0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBL_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 41; DB 1;
Pred. No. 23;
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Mismatches
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MEDLINE=96051385; PubMed=7584024;
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01-NOV-1997 (Rel. 35, Last sequ
                                                               | | :|| || :|: | |
GKTITLEVEGSDNIENVKAKI 30
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                                          GATFQVEVPGSQHIDSQKKAI
Conservative
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                                                                                                                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans
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11 QLMGSQHVDNKEK 23
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                   YP68_CAEEL
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us-09-786-648-4.rsp

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CONFLICT
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                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- DISEASE: ASSOCIATED WITH FAMILIAL HEREDITARY NONPOLYPOSIS COLON
CANCER (HNPCC) (LYNCH SYNDROME). HNPCC IS ONE OF THE MOST COMMON
GENETIC DISEASES IN THE WESTERN WORLD, AND ACCOUNTS FOR 15% OF ALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bronner C.E., Baker S.M., Morrison P.T., Warren G., Smith L.G., Lescoe M.K., Kane M., Earibino C., Lipford J., Lindblom A., Tannergaard P., Bollag R.J., Godwin A.R., Ward D.C., Nordenskjoeld M., Fishel R., Kolodhen R.D., Liskay R.M.; Submitted (OCT-1994) to the EMBL/GenBank/DbBJ databases:
-i- FUNCTION: PROBABLY INVOLVED IN THE REPAIR OF MISMATCHES IN DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
01-0CT-2000 (Rel. 40, Last annotation update)
PMS1 PROTEIN HOMOLOG 2 (DNA MISMATCH REPAIR PROTEIN PMS2).
PMS2 OR PMS12.
Eukor sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Endometrial tumor;

BEDLINE-294552394; PubMed=8072530;
Nicolaides N.C., Papadopoulos N., Liu B., Wei Y.-F., Carter K.C.,
Ruben S.M., Rosen C.A., Haseltine W.H., Fleischmann.R.D.,
Fraser C.M., Adams M.D., Venter J.C., Dunlop M.G., Hamilton S.R.,
Petersen G.M., de la Chapelle A., Vogelstein B., Kinzler K.W.;
"Mutations of two PMS homologues in hereditary nonpolyposis colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 1; Length 386; Pred. No. 28;
SEQUENCE OF 1-191 FROM N.A.
Bookstein C., Edwards C.W., Hulett F.M.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             E -> M (IN REF. 2).
D921F3A0F6845EEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
CONFLICT 191 191 E
SEQUENCE 386 AA; 43830 MW;
                                                                                                                                                                                                                                                                                                        EMBL; D26185; BAA05262.1; -.
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31.28;
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EMBL; Z99104; CAB11802.1;
SubtiList; BG10090; yaan.
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22 IEIPGSEAVKAEKEQV 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 VEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 371:75-80(1994).
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Best Local Similarity
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        and for commercial
                           (See http://www.isb-sib.ch/announce/
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NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
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Interpro; IPR0010386; -.
Fidan, PF0012; HSP70; 1.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS000329; HSP70_2; PARTIAL.
PROSITE; PS01036; HSP70_2; PARTIAL.
PROSITE; PS01036; HSP70_3; PARTIAL.
ATP-binding; Heat shock; Endoplasmic reticulum; Multigene family.
NON_TER 285 288 PREVENT SECRETION FROM ER.
SEQUENCE 288 AA; 31267 NW; 967F5A4A12FA67BF CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Identification of a heat-shock pseudogene from Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 862;
                                                                                                                                                                                               MIM; 6004257,
InterPro; IPR002099; -.
Pfam; PF01119; DNA_MIS_REPAIR_1; 1.
PROSITE; PS00058; DNA_MISMATCH_REPAIR_1; 1.
DNA repair; Disease mutation; Anti-oncogene; Polymorphism.
VARIANT 20 20 (FT1d=VAR_004469.)
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        Usage by
                                                                                                                                                                                                                                                                                                                                                                        170 P -> S (IN REF. 2).
95797 MW; B60A605222CBBCAC CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 40.5; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN D (FRAGMENT).
modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
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MEDLINE-89306577; PubMed-2744444;
Heschl M.F.P., Baillie D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
                                                                                                         EMBL; U13696; AAA63923.1; -. EMBL; U14658; AAA50390.1; -. SWISS-2DPAGE; P54278; HUMAN. MIM; 600259; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.2%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M28528; AAA28076.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TO MAMMALIAN GRP78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 GSQ-HIDSQKKA 20
                                                                                                                                                                                                                                                                                                                                                                                                 862 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSP-4 OR HSP70D
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SEQUENCE FROM N.A.
                                                                                                                                        SEQUENCE FROM N.A.
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    SPAC6G9.02C
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P08979;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPC_BPPHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelab-sib.ch).
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0
                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 39.9 KDA PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.
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0
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          DB 1; Length 288; 30;
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HYPOTHETICAL PROTEIN T15H9.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.7%; Score 40; DB 1; Length 355;
47.4%; Pred. No. 38;
tive 2; Mismatches 8; Indels
                                                          5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 75.4 KBA PROTEIN CGG9.02C IN CHROMOSOME I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95FA4D8E551D9CC2 CRC64;
                                                                                                                                                                                                                                    355 AA
                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
                    Score 40;
Pred. No.
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POLY-GLY.
                                                                                                                                                                                                                                  PRT;
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Pfam: PF01556; DnaJ_C; 1.
PROSITE: PS00036; DNAJ_1; 1.
PROSITE: PS50076; DNAJ_2; 1.
Hypothetical protein; Chaperone;
                                                        9
                                                                                                                                                                                                                                                                            Created)
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                  37.78;
35.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; 247356; CAA87414.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320 TFDVEFPKTELSDEQKAQI 338
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                                                                                                                  CE01664.
                                                                                              3 TFQVEVPGSQHIDSQKK 19
                                                          Conservative
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                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WormPep; T15H9.1; CE0166
InterPro; TPR001623; -.
InterPro; IPR002939; -.
                                                                                                                                                                                                                                                  010005;
01-NOV-1997 (Rel. 35,
Query Match
Best Local Similarity
'-hac 6; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 1
355 AA;
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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  YRY1_CAEEL
Q10005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDH2_SCHPO
Q92347;
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SEQUENCE
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YDH2_SCHPO
ID YDH2_S
AC 092347
DT 01-NOV
DT 01-NOV
DT 01-NOV
DT 01-NOV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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"The repressor gene (c) of the Streptomyces temperate phage phi c31:
mucleotide sequence, analysis and functional cloning.";
Mol. Gen. Genet. 213:269-277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
                                                                                                                                                                                                                                              Murphy L., Harris D., Barrell B.G., Rajandream M.A., Connor R.E.; Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 protein.
655 Aa; 75440 MW; 45E6C4491692DA42 CRC64;
                          Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
REPRESSOR PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ed. No. 73;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  683 AA.
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; 281317; CAB03604.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   535 ATLAVSAPGSHIVDKAWKA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001313; --
Pfam; PF00806; PUF; 5.
Hypothetical protein.
SEQUENCE 655 AA; 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteriophage phi-C31.
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                                                                                     Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA virus
Lambda phage group.
NCBI_TaxID=10719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 9; Conserv
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11

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1199 TFONNVPNYOHIGMKR 1214
                  3 TFQVEVPGSQHIDSQK 18
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MEDLINE-9024573; PubMed-2159623;

MEDLINE-9024573; PubMed-2159623;

Mediss S.R., Space N.J.M.;

Weiss S.R., Space N.J.M.;

The primary structure and expression of the second open reading frame of the polymerase gene of the coronavirus MHV-A59; a highly conserved polymerase gene of the coronavirus MHV-A59; a highly frameshifting mechanism."; an efficient ribosomal frameshifting mechanism."; CONSERVED STRUCTION: THE RNA DEPENDENT RNA POLYMERASE OF CORONAVIRUSES IS A MULTIFUNCTIONAL PROTEIN: IT CONTAINS THE ACTIVITIES NECESSARY FOR THE TRANSCRIPTION EXPRANDED RNA, LEADER RNA, SUBGENOMIC MRNAS AND PROGENT VIRION RNA.

C. CATALITIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine coronavirus MHV (strain A59).
Yluses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
NCBL_TaxID=11142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A polymerase; Helicase; ATP-binding.
POLYMERASE.
CYS/HIS-RICH.
HELICASE.
                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- MISCELLANEOUS: THIS PROTEIN MAY BE TRANSLATED AS A 1A-1B POLYPROTEIN BY A RIBOSOMAL FRAMESHIFTING MECHANISM.
-1- SIMILARITY: TO THE AVIAN CORONAVIRUS IBV RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 1; Length 2733;
Pred. No. 3.4e+02;
2; Mismatches 6; Indels
                                                                                                                                                         37.7%; Score 40; DB 1; Length 683; 50.0%; Pred. No. 76;
                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (BY SIMILARITY).

IN; F3ACC8EF20D20C41 CRC64;
                                                                PIR; S01433; S01433.
Transcription regulation; Repressor; DNA-binding.
SEQUENCE 683 AA; 74077 MW; B02379D204F37D1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (ORF1B).
                                                                                                                                                                                             ..
2
                                                                                                                                                                                                                                                                                                                                                        PRT; 2733 AA.
                                                                                                                                                                                            2; Mismatches
send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X51939; CAA36202.1; ALT_SEQ. PIR; S08652; S08652. PIR; S15760; S15760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA; 309218 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA-directed RNA
                                 EMBL; X12865; CAA31345.1; -. EMBL; X76288; CAA53911.1; -.
                                                                                                                                      Query Match
Best Local Similarity 50.00,
hear 7; Conservative
                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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1506
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86 GRTFDTELTGADHI 99
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase;
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                                                                                                                                                                                                                                                                                                                                                       RRPB_CVMA5
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prognancy.";
Endocrinology 138:4757-4767(1997).
-i- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
INCLUDING JAKS, TYKZ, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -! TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT CONCEPTUS AT DAY 15 OF PREGNANCY. -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS. -!- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
INRI_SHEEP STANDARD; PRT; 560 AA.

028589; 095206;
01-NOV-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
INTERFERON ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)
(INTERPERON ALPHA/BETA RECEPTOR-1).
                                                                                                                                    Ovis aries (Sheep).
Eukaryota: Metazooa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinee; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE-98006426; PubMed-9348203; Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.; Molecular cloning of ovine and bovine type I interferon receptor subunits from uteri, and endometrial expression of messenger ribonucleic acid for ovine receptors during the estrous cycle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
INTERFERON-ALPHA/BETA RECEPTOR ALPHA
                                                                                                                                                                                                                                                                                     Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F., "Structure of an ovine interferon receptor and its expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                        Mol. Endocrinol. 17:207-215(1996).
                                                                                                                                                                                                                                                         TISSUE=Endometrium;
MEDLINE=97135690; PubMed=8981227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X95939; CAA65183.1; -. EMBL; U65978; AAB84231.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   437
458
560
84
220
47
47
55
85
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Pfam; PF00041; fn3; 1
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Endometrium;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                       NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
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438
459
76
199
                                                                                                                     IFNAR1 OR IFNAR
                                                                                                                                                                                                                                                                                                                        endometrium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor;
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TRANSMEM
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CARBOHYD
CARBOHYD
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Gaps

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2; Mismatches

8; Conservative

37.7%; 50.0%;

Freier U.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C., Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.; "The genome sequence of the thermoacidophilic scavenger Thermoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acidophlum.";
Nature 407:508-513(2000).
-1- FUNCTION: BINDS TO THE SIGNAL SEQUENCE OF PRESECRETORY PROTEIN
WHEN THEY EMERGE FROM THE RIBOSOMES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                 Plant MOL. Biol. Rep. 13:336-342(1995).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE TATC FAMILY.
                                                                                         Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
NCBL_TaxID=2839;
                                                                                                                                                                                                                                       Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Frei
"The chloroplast genome of a chlorophyll a+c-containing alga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Archaea; Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL: 25083364F2A89E88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002033; -. Pfam, PF00902; UPF0032] Pfam, PF00912; UPF0032] Trans: 1. Chloroplast; Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-007-2000 (Rel. 40, Created)
01-007-2000 (Rel. 40, Last sequence update)
01-007-2000 (Rel. 40, Last annotation update)
01-007-2000 (Rel. 40, Last annotation update)
SIGNAL RECOGNITION 54 KDA PROTEIN (SRPS4).
     HYPOTHETICAL 30.1 KDA PROTEIN YCF43 (ORF263).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   456 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
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POTENTIAL.
POTENTIAL.
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MEDLINE=20479972; PubMed=11029001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30080 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 267753; CAA91737.1; -. Mendel; 5328; ODOsi; ycf43;1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :|:||:||: |: |: 31 TVTLELPFSEHIEELKQRL 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thermoplasma acidophilum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
'-has 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213
241
263 AA;
                                                                                                                                                                                                                                                                                                Odontella sinensis.
                                                         Odontella sinensis
                                                                                                                                                                                                                 SEQUENCE FROM N.A. Kowallik K.V., Sto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                    Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SR54_THEAC
Q9HKT0;
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TRANSMEM
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          SO THE THE TANK TO THE TANK TO
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MEDLINE-92024080; Pubmed-1926776;
Pallm P., Schleper C., Grampp B., Yeats S., McWilliam P., Reiter W.-D.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfolobus virus-like particle SSV1.
Viruses; dsDNA viruses, no RNA stage; Fusellovirus.
                                                                               (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                           (POTENTIAL)
                                                                                                                                                                                                                    (POTENTIAL)
                                (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                       -> G (IN REF. 2).
-> D (IN REF. 2).
E7198A1905D4805C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete nucleotide sequence of the virus SSV1 of the archaebacterium Sulfolobus shibatae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .l protein.
112 AA; 13204 MW; 23F9C02D979AF383 CRC64;
                                                                                                       (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
N-LINKED (GLCNAC...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
HYPOTHETICAL 13.2 KDA PROTEIN (ORF F-112).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 33, Created)
(Rel. 33, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          112 AA
                                                                                                                                                                                                                                                                                                                                                                    Score 39.5; D. Pred. No. 74; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ATFQV-----EVPGSQHIDSQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 ADYQILGTDNWKKLPGCQHITSSK 83
                                                                                                                                                                                                                                                                                              ΨM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | |:: || ::| ||| 31 AQFEISVPSAYNIQRALKAI 50
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X07234; CAA30220.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virology 185:242-250(1991).
                                                                                                                                                                                                                                                                                              63918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                  313
359
377
434
352
522
560 AA;
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Hypothetical protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
hes 8; Conserv
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P49538;
01-FEB-1996 (
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 20
Y13K_SSV1
ID Y13K_SSV1
AC P20220;
                                                                                                       CARBOHYD
CARBOHYD
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CONFLICT
                                CARBOHYD
                                                         CARBOHYD
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YC43_ODOSI
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Best Loca Matches

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4444

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Gaps

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Length 263; Indels

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DOMAIN
TRANSMEM
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SEQUENCE
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                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                    CHAIN
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    g
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                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                      ö
-!- SUBUNIT: ARCHAEAL SIGNAL RECOGNITION PARTICLE CONSISTS OF A 7S RNA MOLECULE OF 300 NUCLEOTIDES AND TWO PROTEIN SUBUNITS: SRF54 AND SRP19 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-!- DOMAIN: HAS A TWO DOMAIN STRUCTURE: THE G-DOMAIN BINDS GTP; THE M-DOMAIN BINDS THE 7S RNA IN PRESENCE OF SRP19 AND ALSO BINDS THE SIGNAL SEQUENCE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SRP FAMILY OF GTP-BINDING PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -: FUNCTION: RECEPTOR FOR INTERLEUKIN-7.
-: SUBGNIT: HETERODIMER OF AN ALPHA CHAIN AND A COMMON GAMMA CHAIN.
-: SUBCELLUAR LOCATION: TYPE I MEMBRANE PROTEIN.
-: TISSUE SPECIFICITY: SPLEEN; TYPMUS; AND FETAL LIVER.
-: SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-: SIMILARITY: CONTAINS I FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goodwin R.G., Friend D., Ziegler S.F., Jerzy R., Falk B.A., Gimpel S., Cosman D., Dower S.K., March C.J., Namen A.E., Park L.S. "Cloning of the human and murine interleukin-7 receptors: demonstration of a soluble form and homology to a new receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
INTERLEUKIN-7 RECEPTOR ALPHA CHAIN PRECURSOR (IL-7R-ALPHA).
                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                Signal recognition particle; GTP-binding; RNA-binding.
DOMAIN 1 289 G-DOMAIN (BY SIMILARITY).
DOMAIN 290 456 M-DOMAIN (BY SIMILARITY).
NP_BIND 104 111 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                E6560FA972DA3EA7 CRC64;
                                                                                                                                                                                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                      (BY
(BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=90199875; PubMed=2317865;
                                                                                                                                                                                                                                                                                                                      GTP
                                                                                                                                                                                                                                    EMBL; AL445064; CAC11655.1; -.
                                                                                                                                                                                                                                                                                                                                                51080 MW;
                                                                                                                                                                                                                                                                                                                                                                                         36.8%;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match 36.8
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                   PROSITE; PS00300; SRP54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                         \frac{111}{188}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                superfamily.";
Cell 60:941-951(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 IPGSQKIDDSK 363
                                                                                                                                                                                                                                                                                        290
104
184
184
242
456 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                8 VPGSQHIDSQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IL7R_MOUSE
P16872;
                                                                                                                                                                                                                                                                                                                                    NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                      NP_BIND
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  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
T-CELL SURFACE GLYCOPROTEIN CD5 PRECURSOR (LYMPHOCYTE GLYCOPROTEIN LY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                SER/THR-RICH.

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

PHOSPHORYLATION (BY PKC) (POTENTIAL).

CC06A5CE95543849 CRC64;
                                                                                                                                                                                                                                             INTERLEUKIN-7 RECEPTOR ALPHA CHAIN
                                                                                                                                                                        Receptor; Transmembrane; Glycoprotein; Phosphorylation; Signal. SIGNAL 1 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal, Transmembrane, Glycoprotein; T-cell.
SIGNAL
1 23 BY SIMILARITY
CHAIN 24 491 T-CELL SURFACE GLYCOPROTEIN CD5.
DOMAIN 25 368 EXTRACELLULAR (POTENTIAL).
TRANSMEM 369 398 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 1; Length 459;
Pred. No. 72;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murakami T.;
Submitted (JUL-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY ACT AS A RECEPTOR IN REGULATING T-CELL
-PROLIFERATION. CD5 INTERACTS WITH CD7/2/LYB-2.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: CONTAINS 2 SRCR DOMAINS.
                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00530; SRCR; 3.
PROSITE; PS00420; SRCR_1; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1) (LYT-1) (LYMPHOCYTE ANTIGEN CD5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequ
30-MAX-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.8%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D10728; BAA01571.1; -.
EMBL; M29697; AAA39304.1;
PIR; D34791; D34791.
MGD; MGI:96562; Il7r.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                     InterPro; IPR000950; -.
InterPro; IPR00177; -.
InterPro; IPR002465; -.
Pfam; PF00041; fn3; 1.
                                                                                                                                                                                                                         20
233
2539
264
459
189
1189
1115
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                                                                                                                                                                                                                                                                       21
240
265
128
184
60
115
177
282
459 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 QVEVPGSQHI 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 QLEVDGSQHL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-89356251; PubMed-2766926;
Heschl M.F.P., Baillie D.L.;
"Characterization of the hsp70 multigene family of Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0301; HEATSHOCK70.
PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Endoplasmic reticulum; Multigene family;
                                                                       POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
88DD76F8E6891CDE CRC64;
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                         1; Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.8%; Score 39; DB 1; Length 661; 35.3%; Pred. No. 1.1e+02; tive 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
HEAT SHOCK 70 KDA PROTEIN C.
HEAVENT SECRETION FROM ER.
7F5CD624F48293BA CRC64;
                                                                                                                                                                                                                                                                                                           3; Indels
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN C PRECURSOR.
                                                                                                                                                                                                                                            DB 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        661 AA
                                                                                                                                                                                                                                                      Score 39; DB Pred. No. 78; 4; Mismatches
                       SRCR 1.
SRCR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                 Ξ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M26604; AAA.28074.1; -.
PIR; A32475; A32475.
HSSP; P19120; INGJ.
InterPro; IPR0010886; -.
InterPro; IPR001023; -.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 P
                                                                                                                                                                                                                                                         36.8%;
46.2%;
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                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                        | | | | : |:|::
436 QVENPAASHVDNE 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
                                                                                                                                                                                                                                 Query Match
Best Local Similarity 4
                                                                                                                                                                                                                                                                                                                                                        5 QVEVPGSQHIDSQ 17
                                                                                                                            176
239
491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
658
661 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 25
HS7C_CABEL
AC P27420;
DT 01-AUG-1992
DT 01-AUG-1992
DT 01-AUG-1992
DT 15-JUL-1998
OS CAENORYA
OC BURATYOLE;
MCDL TAXID=6
RN [1]
RN [1]
RN [1]
RN [1]
RA HESP-3 OR HESP-3
OX WCBL_TAXID=6
RN [1]
RN [1]
RN [1]
RA HESP-1 ON HESP-3
CC CHADLINE—8935
RA HESP-3 ON HESP-3
CC TAIS SWISS-P
CC THIS SWISS
                       DOMAIN
DOMAIN
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CARBOHYD
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CARBOHYD
SEQUENCE
DOMAIN
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Gaps

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505 TFEIDVNGILHVTAEDK 521
3 TFQVEVPGSQHIDSQKK 19
                     Q
ò
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Search completed: July 16, 2001, 16:44:04 Job time: 463 sec

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July 16, 2001, 16:43:37; Search time 57.41 Seconds (without alignments) 48.396 Million cell updates/sec
                                                                                                                                                                                      425026
       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                     hits satisfying chosen parameters:
                                                                                                                                                                  425026 seqs, 132305027 residues
                                            OM protein - protein search, using sw model
                                                                                                                    1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                  US-09-786-648-4
                                                                                                                                                                                     Total number of
                                                                                                            Perfect score:
                                                                                                                                       Scoring table:
                                                                                                                      Sequence:
                                                                                                                                                                  Searched:
                                                             Run on:
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09hb36 Anno sapien 042099 cyprinus ca 09pka3 chlamydia m 09hca3 homo sapien 09h350 homo sapien 09jri4 neisseria m 09jri4 neisseria m 09gri4 neisseria m

022511 vitis vinif Q43098 psophocarpu Q97690 leishmania Z027066 methanobact Q9f517 zymomonas m Q91y67 arabidópsis Q9ksz baciltús ha Q9sxm5 glyčine max Q9syg9 gfycine max Q9shg6 knoo sapien

022511 043098 0987906 027066 027066 097517 098922 098922 098922 098922 098923 099836 04209 04209 099938 0997814 0997816 0997816

2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005 2005

091529 hepatitis b 09qmn7 hepatitis b 093442 caenorhabdi 09vgt2 drosophila 09v1b9 drosophila 0917m2 drosophila

Q9SQ79 O91529 Q9QMN7

40.5 40.5

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

# ALIGNMENTS

RESULT

Q57193 ID Q57193 PRELIMINARY; PRT; 124 AA.	Q57193; 01-NOV-1996	DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)	CHOLERA TOXI	_	-	OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.	ON NUCEL_TAXID=000;	KN LIJ		_	Dams E., De Wolf M., Dierick W.;	RT "Nucleotide sequence analysis of the CT operon of the Vibrio cholerae	-	RL Blochim. Blophys. Acta 1090:139-141(1991).	RP SEQUENCE FROM N.A.		RA Shi C., Cao C., Zhang J., Ma Q.;			٠,	RC STRAIN-CLASSICAL BIOTYPE 569B;	•	٠.	_	_	DR EMBL; A00931; CAA00098.1;	Ξ.	•	_	DR PRINTS; PR00772; ENTEROTOXINB.	_	Signal.	SIGNAL 1 21	FT CHAIN 22 124 CHOLERA TOXIN B PROTEIN (CTB).
									ince to have a	sult being printed,	thution.				Description	***********	Q57193 vibrio chol	Q56635 vibrio chol	Q9rp15 vibrio chol	Q9r646 vibrio chol	Q9ljb0 arabidopsis	Q99987 homo sapien	Q91gm2 oryza sativ	Q40742 oryza sativ	Q9nkd5 drosophila	Q9p4e0 ustilago ma	049876 lupinus alb	Q9u3m9 caenorhabdi	Q9sxc9 arabidopsis	Q9pky2 chlamydia m	Q9syf4 arabidopsis	Q9qz17 mus musculu	Q9n136 ovis aries	P97431 mus musculu

Q57193 Q56635 Q9RP15

100.0 100.0 100.0 94.3 49.1 46.2 46.2

106 106 106 100 52 51 51 49 48 48

Query Match Length DB

Score

Result No.

09R646 09L980 099987 09LGM2 040742 09P4E0 069P4E0 069P4E0 09SXC9 09SXC9 09SXC4 09SXC4 09SXC4 09SXC4 09CXC4 09CXC4

10

428 392 395 1166 293 374 574 374 310

43.4 42.0 42.0 41.5 41.5 41.5 41.5

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

sp_unclassified:*
sp_vertebrate:*
sp_virus:*

sp_invertebrate:*

sp_mammal:* sp_human:*

sp_mhc:*

sp_archea:* sp_bacteria:*

sp_fungi:*

SPTREMBL_16:*

Database

sp_organelle:*
sp_phage:*
sp_plant:*

sp_rodent:*

112::41

Gaps

ö

Length 124;

RESULT Q56635

g

```
"Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety P1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakashima K., Eguchi Y., Nakasone N.; "Characterization of an enterotoxin produced by Vibrio cholerae
Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
SEQUENCE 124 AA; 13905 MW; 23BF83FFF793E5B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Microbiol. Immunol. 39:87-94(1995).
HSSP; P01556; 1XTC.
InterPro; IPR001835; --
Pfam: PF01376; Enterotoxin_B; 1.
PRIMTS; PR00772; ENTEROTOXINB.
SEQUENCE 103 AA; 11645 MW; 992A05C077F2F70E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
EMB|CAB77996.1.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.3%; Score 100; DB 2; I larity 95.2%; Pred. No. 2.4e-09; Conservative 0; Mismatches 1;
                                                                                    Score 106; DB 2;
Pred. No. 2.9e-10;
Mismatches 0;
                                                                                                                                                                                                                                                                                   103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            552 AA
                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TIEMBLREL 13, Created)
01-MAY-2000 (TIEMBLREL 13, Last seq
01-0CT-2000 (TIEMBLREL 15, Last ann
CHOLERA-LIKE ENTEROTOXIN B SUBUNIT.
                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
MEDLINE=95303036; PubMed=7783690;
                                                                                      100.0%; Sc
100.0%; Pr
tive 0;
                                                                                                                                                                              66 GATFOVEVPGSQHIDSQKKAI 86
                                                                                                                                                            1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 GAIFQVEVPGSQHIDSQKKAI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                      Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae
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                                                                                          Query Match
                                                                                                                                                                                                                                                                               09R646
09R646;
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Q9R646
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                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRATN=KNIH002;
Shin H.J., Park Y.C., Kim Y.C.;
Shin H.J., Park Y.C., Kim Y.C.;
"Cloning and nucleotide sequence analysis of the virulence gene cassette from Vibrio cholerae KNIH002 isolated in Korea.";
Misainmurhag Hoiji 35:205-210(1999).
BMBL SAF175708; AAD31360.1;
InterPro; IPR001835;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=S7;
Yamamoto K., Do V.G., Xu M., Iida T., Miwatani T., Albert M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Comparison of cholera toxin genes (ctxAB) of non-Ol vibrio strains 854 (0139-bengal) and S7 (037) from two outbreaks."; Submitted (ApR-1994) to the EMBL/GenBank/DDBJ databases. EMBL; D30052; BAA06289.1; -- HSSP; P01556; 2CHB.
                                     Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 124;
                                                                      Indels
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3F87B2F297953179 CRC64;
                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                  Score 106; DB 2;
Pred. No. 2.9e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 106; DB 2;
100.0%; Pred. No. 2.9e-10;
Live 0; Mismatches 0;
                                                                                                                                                                                                                               124 AA
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                                                                    Mismatches
                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001835; -
Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
PRODOM; PD012805; -; 1.
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                                  100.0%;
100.0%;
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13871 MW;
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                                                                                                                        66 GATFQVEVPGSQHIDSQKKAI 86
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                                                                                                      1 GATFQVEVPGSQHIDSQKKAI
                                                                    Conservative
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Matches 21; Conservative
                                                                                                                                                                                                                             PRELIMINARY;
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                                  Query Match
Best Local Similarity
Matches 21; Conserv
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SEQUENCE
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Q56635;
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**09RP15**; Q9RP15

RESULT Q9RP15

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Gaps

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Length 103; Indels ő

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P SEQUENCE FROM N.A.
C STRAIN-CV. NIPPONBARE;
A SASAKI T., MATSUMOTO T., YAMAMOTO K.;
A CATLA anipponbare(GA3) genomic DNA, chromosome 1, PAC anippons of the concerpond of th
                                        basaki T., Matsumoto T., Yamamoto K.;
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
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                                                                                                                         clone:P0041E11.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TFQVEVPGSQHIDSQKKAI 21
        STRAIN-CV. NIPPONBARE;
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Q9NKD5
ID Q9NKD5
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                                                Sasaki
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MEDLINE-9800821; PubMed-9344656;
MEZU J., Oku A., Jones M.H., Shimane M.;
MEZU J., Oku A., Jones W.H., Shimane M.;
"Identification of two novel human putative serine/threonine kinases,
VRK1 and VRK2, with structural similarity to vaccinia virus B1R
                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                      Length 552;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00220; S_TKC; 1.
ATP-binding; Serine/threonine-protein kinase; Transferase.
SEQUENCE 508 AA; 58126 MW; 157FBF8F48511AF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics 45:327-331(1997).
-!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL: AB000450; BAA19109.1; -.
                                                                                                                                                                                                                                                                                                                   Indels
TAC and BAC clones.";
DNA 7:217-221(2000).
EMBL, RESO06066; BAB01195.1; -
SEQUENCE 552 AA; 63036 MW; 740EA16CDEBB2447 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ESTS AU056822($20908).
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Last annotation update)
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                                                                                                                                                                                                                                  Score 52; DB 10;
Pred. No. 1.9;
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                                                                                                                                                                                                                                                                                                               2; Mismatches
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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                                                                                                                                                                                                                                  49.18;
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147 QVEIPASMEIDEETKAI 163
                                                                                                                                                                                                                              Query Match 49.1
Best Local Similarity 58.8
Matches 10; Conservative
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SEQUENCE FROM N.A.
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Q9LGM2;
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ID Q9
O9 DT Q9
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
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MEDILINE-97569379; PubMed-9225866;

Schultz T.F., Quatrano R.S.;

"Characterization and expression of a rice RAD23 gene.";

Plant Mol. Biol. 34:557-562(1997).

EMBL; UG5330; AAB65841.1;

HSSP; P02248; ITBE.
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                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   395 AA.
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                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
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SMART; SM00165; UBA; 1.
SEQUENCE 392 AA; 41753 MW; BD0
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InterPro; IPR000449; -.
InterPro; IPR000626; -.
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10 GSTFQIEVDSAQKVADVKRII 30
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Pfam; PF00240; ubiquitin; 1.
Pfam; PF00627; UBA; 2.
| :|| || || || || 1
183 TTATKVPGGWHIDGQKRWI 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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e description

us-09-786-648-4.rspt

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InterPro; IPR00119; -.
InterPro; IPR002290; -.
InterPro; IPR002290; -.
Pfam; PF00069; PAthase; 1.
PRINTS; PR00130; ANTIFREEZEI.
PROSITE; PS001107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS001108; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                           IPR000159;
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Best Local Similarity
1.2 8, Conserve
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     InterPro;
                           InterPro;
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049876
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     DAR DOR DAR SWEET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STARIN-Y, CN BW SP.
STRAIN-Y, CN BW SP.
Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefl A.R., Moshrefl M.,
Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
Sethil H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AE003408; ARF44847.1; --
Flybase; Fegnolo28907; BG:DS01514.3.
                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-Y, CN BW SP;
MEDLINE-99403001; PubMed=10471707;
Ashburner M., Mista S., Roote J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Celniker S., Rubin G.M.;
An exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster: the Adh region.";
Genetics 153:179-219(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andrews D.L., Egan J.D., Mayorga M.E., Gold S.E.;
"The Ustilago maydis ubc4 and ubc5 genes encode members of a MAP
kinase cascade required for filamentous growth.";
Mol. Plant Microbe Interact. 13:781-786(2000).
--- SIMILARITY: TO THE SER/THR FAMILY OF PROFEIN KINASES.
EMBL; AF197562; AAF86841.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
NCBL_TaxID=5270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Length 395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .i protein.
395 AA; 43561 MW; AE4F1CC4ADD3DA73 CRC64;
                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 43.6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PHEROMONE-RESPONSIVE MAPKK KINASE UBC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 47; DB 5
Pred. No. 9;
2; Mismatches
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STRAIN=1/2;
MEDLINE=20331594; PubMed=10875339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ustilago maydis (Smut fungus).
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Best Local Similarity 56.2
Matches 9; Conservative
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329 RVSVPGSTHIDADANA 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                     BG:DS01514.3.
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SEQUENCE 33
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Q9P4E0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09P4E0;
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                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MR-2001 (TrEMBLrel. 16, Last annotation update)
CLASS III CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
CHIBI OR LUPA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lupinus albus (White lupine).

Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Enganoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;

Fabales; Fabaceae; Papilionoideae; Lupinus.

NCBL_TaxID=3870;
PROSIE, ECCET, SMOO20; SIRC; 1.
ATP-binding; Kinase; Scrine/threonine-protein kinase; Transferase.
epongrammer 1166 AA; 123298 MW; A89E0019AABD4172 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                      3; Length 1166;
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                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. ULTRA;
Regalado A.P., Vladal S., Neves A.; Ricardo C.P.P.,
Rodrigues-Pousada C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
; DB1B21728F657F2F CRC64;
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                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                              293 AA.
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                                                                                                                      43.9%; Score 46.5; I
47.6%; Pred. No. 35;
Live 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                              PRT;
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HSSP, P23472; 2HVM.
Mendel; 28297; Lupal; Chibl; 28297.
InterPro; IPR001579; -...
Pfam; PF00192; chitinase_2; 1.
PROSITE; PS01095; CHITINASE_18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                   2 ATFQVEVP-GSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GATFOVEVPGSOHIDSOKKAI 21
                                                                                                                      Query Match
Best Local Similarity 47.6
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Q9U3M9;
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ID 09
AC 09
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C40H5.3.

White

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SEQUENCE FROM N.A.
STRAINE-MOPN / NIGG;
MEDLINE-2015/0255, PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Li J., Kremenetskaia I., Luros J., Ngan i., Gonzalez A., Altafi H.,
Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Huizar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome I BAC F15I1 sequence.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR000626;
                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41.5%; Score 44; DB 10; Length 91;
47.6%; Pred. No. 5.8;
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Last annotation update)
                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                             Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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; Pred. No. 22;
3; Mismatches
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EMBL; AE002300; AAF39192.1; -.
                                                                                                   Created)
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                                                             PRT;
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374 AA; 41218 MW;
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                                                                                                 (TrEMBLrel. 15,
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                                                                                                                                                         HYPOTHEFICAL PROTEIN TC0328
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Best Local Similarity 48.09
Watches 12; Conservative
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Matches 10; Conservative
                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae AR39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
                                                                                               01-OCT-2000
01-OCT-2000
01-MAR-2001
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Q9SYF4;
                                                                               Q9PKY2;
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                     RESULT
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Vysociskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Vysociskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Chee J.M., Liu A., Li J., Gonzalez A., Liu K., Vaysberg M., Sakano H.,
Chin C., Howng B., Choi E., Chiou J., Altafi H., Araujo R., Brooks S.
Buehher E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Paraller L., Khan S., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
Paralidopsis Lhaliana chromosome I BAC T17H3 sequence.";
Submitted (AUG.1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AC005916, AAD45990.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                               Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C.elegans: A platform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR001382; -.
Pfam; PF01532; Glyco_hydro_47; 1.
PRINTS; PR00747; GLYHDRLASE47.
SEQUENCE 574 AA; 65707 MW; 4ACC456DE487EA93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        67D202886D6A7824 CRC64;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
C40H5.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
T17H3.2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB F
12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 574 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                43.4%; Score 46; 42.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                          MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                              investigating biology.";
Science 282:2012-2018(1998).
EMBL; 281482; CAB03954.2; -
SEQUENCE 374 AA; 42198 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 GVEFHIWFPGQPHADEQKE 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GATFQVEVPGSQHIDSQKK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TFQVEVPGSQHIDSQKK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 43.4
Best Local Similarity 42.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 58.8
Matches 10; Conservative
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                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                       NCBI_TaxID=6239;
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Q9SXC9; 698XC9

RESULT 13 69SXC9

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NCBI_TaxID=3702

Query Match

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Length 467; Indels

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SEQUENCE FROM N.A.
MEDLINE-96127529; Pubmed-8590279;
MEDLINE-96127529: A. Sato S., Kotani H., Sazuka T., Miyajima N.,
Sugiura M., Tabata S.,
"Sequence analysis of the genome of the unicellular cyanobacterium
                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB-COLON, KIDNEY, GENOMIC DNA 129/J STRAIN (DR. J. ROSSANT);
Grossman A., Mittrucker H.W., Antonio L., Mak T.W.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U73029; AAB36714.1; -.
HSSP; P23906; 2IRP.
MGD; MGI:1859211; Irf6.
Interpro: IPRO01346; -.
Pfam; PF00605; IRR: 1.
PRINTS; PR00267; INTFRNREGFCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tabata S.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prodom; P000235; ; 1.
PROSITE; PS00601; IRF; 1.
SMART; SM0348; IRF; 1.
SEQUENCE 467 AA; 53106 MW; 68CCAA90680FEDC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
NCBL_TaxID=1148;
                                                                                                                                                                                                                 01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 179.7 KDA PROTEIN.
 ;
9
                                                                                                                                                                                  467 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB:
Pred. No. 35;
6; Mismatches
DB
35;
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35;
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                                Mismatches
Score 44;
Pred. No. 3
                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                    INTERFERON REGULATORY FACTOR 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41.5%;
41.5%;
                                                                                    ||: || :|| :|: :
273 QVKFPGPEHITNEKQKL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          273 QVKFPGPEHITNEKQKL 289
                                                              5 QVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 QVEVPGSQHIDSQKKAI 21
               Best Local Similarity 41.2
Matches 7; Conservative
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Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-BALB/C;
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 Query Match
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                                                                                                                                                                                P97431
P97431;
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P97431
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Pred. No. 24;
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                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=129/J;
Sands A., Mak T.W.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF177668; AAF00915.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE-15 DAY PRECNANT UTERUS;
Choi Y., Spencer T.E., Bazer F.W.;
"Cloning and Analysis of Ovine IRF-6.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF228446; AAF34782.1;
InterPro; IPR001346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00348; IRF; 1.
SEQUENCE 467 AA; 52970 MW; 21E04F749844D88F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   330 AA; 37355 MW; EB02EC8B751CBD7D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 16, Last annotation update)
INTERFERON REGULATORY FACTOR 6.
Ovis aries (Sheep).
                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                  330 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467 AA
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                                                                                                                                                   Created)
                                                                                                                  PRT;
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PRINTS, PRODGEGF; INTFRINEGFCT.
PROSITE; PS00601; IRF; 1.
SMART; SM00348; IRF; 1.
1 GATFQVEVPGSQHIDSQKKAI 21
                   58 GKTFNLEVKGSEIIQOVKNMI 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00605; IRF; 1.
PRINTS; PR00267; INTERNEGECT.
PRODOM; PD002355; -; 1.
PROSITE; PS00601; IRF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.5%;
41.2%;
                                                                                                                                  0902L7;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||: || :|| ::|: 250 QVKFPGPEHITNEKQKL 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                  PRELIMINARY;
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                  IRF6 (FRAGMENT).
IRF6.
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NON_TER
SEQUENCE
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                                                                                                                090ZL7
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Q9N136
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Q9QZL7
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Gaps

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233 GRPFIPEIPGSEHAIDS 249

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RESULT 21

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                                                                                                                                                           Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Spermatophyta;
Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome."; DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-CV. THOMPSON SEEDLESS (CLONE 2A); TISSUE-FRUIT;
Cassol T., Adams D.O.;
Submitted (AUG-1977) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: FAD (BY SIMILARITY).
-!- SIMILARITY: TO PYRIDINE NUCLEOTIDE-DISULPHIDE OXIDOREDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; Vitis
NCBL_TaxID=29760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 2; Length 1742;
Pred. No. 1.5e+02;
4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002048; -.
PROSITE; PS0018; FE_HAND; UNKNOWN_4.
Hypothetical protein.
SEQUENCE 1742 Aa; 179710 MW; 56C815A887D30B82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FAD; Flavoprotein; Oxidoreductase; Redox-active center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B26113AE09A121DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAKR-2001 (TrEMBLrel. 16, Last annotation update)
GLUTATHIONE REDUCTASE (NADPH) (EC 1.6.4.2) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4; Mismatches
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PRINTS; PR00469; PNDRDTASEII.
PROSITE; PS00076; PYRIDINE_REDOX_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF019907, AAB70837.1; -. HSSP; P00390; 1ALG. Mendel; 26381; Vitvi;1190;26381. InterPro; IPR000103; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GGTFSIDVPGSALVADPDRTI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60695 MW;
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InterPro; IPR001327; -.
Pfam; PF00070; pyr_redox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 38.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 58.8
Matches 10; Conservative
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022511
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1 GATFQVEVPGSQH-IDS 16

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SEQUENCE FROM N.A.
MEDLINE-98249626; PubMed=9588027;
Basa M., Teramoto T.;
"cDNA cloning, gene expression and secretion of chitinase in winged
                                                                                                                                                                                                                                                             Plant Cell Physiol. 39:349-356(1998).
-!- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                               Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
Eukaryota; Viridiplantea; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae, Papilionoideae; Psophocarpus.
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-FRIEDLIN;
MEDLINE-98146435; PubMed-9477341;
Ivens A.C., Lewis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 10; Length 298;
Pred. No. 31;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A physical map of the Leishmania major Friedlin genome.";
Genome Res. 8:135-145(1998).
EMBL; AL139794; CAC22649.1; -.
                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001579; -.
Pfam; PF00192; Chitinase_2; 1.
PROSITE; PS01095; CHITINASE_18; 1.
Glycosidase; Hydrolase.
SEQUENCE 298 AA; 31557 MW; 675D1379D46424E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                         01-NOV-1996 (TIEMBLE). 01, Last sequence update) 01-MAR-2001 (TIEMBLE). 16, Last annotation update) CHITINASE (EC 3.2.1.14).
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298 AA
                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
PRT;
                                                                                                                                                                                                                                                                                                        EMBL; D49953; BAA08708.1; -. HSSP; P23472; ZHVW. Mendel; 1633; Psote;Chib1;1633.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 GVDFDIESGGSNHYDDLARAL 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
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Best Local Similarity 38.1%;
Matches 8; Conservative
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                            01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GATFOVEVPGSOHIDSOKKAI
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PRELIMINARY;
                            01-NOV-1996 (TrEMBLrel.
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SEQUENCE FROM N.A.
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                                                                                                                                                              NCBI_TaxID=3891;
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043098
               043098
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NCBI_TaxID=542;
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Q9LY67
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                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09F5L7;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
17-MA GUNINE TRANSGLYCOSYLASE.
Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonas group;
                                                                                                                                                                                                                                                                                                 Archaea; Buryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanothermobacter.
NCBI_TaxID=145262;
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Pred. No. 39;
6; Mismatches 6; Indels
                                                                        5; Length 356
                                                                                                5; Indels
                                      356 AA; 39755 MW; FE5C8A120287F299 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50C56FE519290714 CRC64;
                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 16, Last annotation update)
SENSORY TRANSDUCTION HISTIDINE KINASE.
                                                                        Score 43; DB 5
Pred. No. 38;
6; Mismatches
                                                                                                                                                                                                         365 AA.
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                                                                                                                                                                                                                                                                                        Methanobacterium thermoautotrophicum
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Interpro, IPR002123; Pfam; PF01553; Acyltransferase; 1.
Transferase.
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MEDLINE-98037514; PubMed-9371463;
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49 AIFLVKIPGGELVDANRSA 67
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                                                                      Ouery Match 40.6's
Best Local Similarity 38.9'
Matches 7; Conservative
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Best Local Similarity 36.8
Matches 7; Conservative
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                                       SEQUENCE
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09F5L7
1D 09F5L7
AC 09F5L7
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OS Zymomo
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                                                                     "Sequence analysis of 44B6 fosmid clone of Zymomonas mobilis ZM4.";
Submitted (COT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF313764; AAG29862.1; - SEQUENCE 399 AA: 44287 AW; 75CEF229E70F94A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Schaefer M., Mewes H.W., Rudd Heger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W., Rudd Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                             Length 399;
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ALIG3818; CAB87801.1;
INTERPT: IRRO01752;
Pfam; PF00225; Kinesin; 2.
PRINTS; PR00380; KINESINHEAVY.
PROSITE; PS00401; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00129; KISC; 1.
ATP-binding; Coiled coil; Microtubules; Motor protein.
SEQUENCE 439 AA; 49028 MW; 9BD55085A1966D70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                       Pred. No. 43;
7; Mismatches
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Job time: 472 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Best Local Similarity 38.1
Matches 8; Conservative
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                                               Ahn J.Y., Kang H.S.;
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Best Local Similarity
'-has 8; Conservē
SEQUENCE FROM N.A.
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GenCore version 4.5

	Copyright (c) 1993 - 2000 Compugen Ltd.
OM protein - pro	OM protein - protein search, using sw model
Run on:	July 16, 2001, 16:35:41; search time 56.06 Seconds (without alignments) 22.710 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-786-648-5 107 1 GETRQVEVPGSQHIDSQKKAI 21
Scoring table:	BLOSUM62 Gapop 10.0 , Gapext 0.5
Searched:	412676 seqs, 60623988 residues
Total number of	Total number of hits satisfying chosen parameters: 412676
Minimum DB seq Maximum DB seq 1	Minimum DB seq length: 0 Maximum DB seq length: 2000000000
Post-processing.	Post-processing: Minimum Match 00% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_0601:*

| SIDSS/gcgdata/geneseq/geneseqp/AA1980.DAT:*
| SIDSS/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDSS/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ADP-ribosylating t Escherichia coli v E. coli heat-labil Recombinant exotox Labile toxin (LT-B Recombinant exotox Recombinant exotox coli verotoxin-1 Recombinant exotox E. coli heat labil Heat labile toxin Description ы AAW95226 AAY68365 AAB66239 AAB73243 AAB73244 AAY01300 AAY87463 AAR72545 AAB73241 AAB73242 AAY41816 ü 22 22 22 22 22 22 22 22 22 23 DB Query Match Length 93393 134 142 155 163 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 Score 107 107 107 107 107 107 107 107 Result Š.

C. jejuni flagelli	Cholera toxin B/en	Synthetic cholera	Heat labile entero	Cholera toxin B su	Cholera toxin B su	Amino acid sequenc	Cholera Toxin B-su	B subunit of the h	Cholera toxin B su	Amino acid sequenc	Plant-optimized E.	LTB-CTB fusion pro	Sequence of LT-B-M	LTB-CTP fusion pro	HSV-1 antigen/heat	Sedneuce of snp-nu	Plant-optimized V.	GtfB.1/CTB chimeri	Network polymer wh	B subunit of CT.	Adhesin/V.cholerae	Helicobacter pylor	Helicobacter pylor	Network polymer wh	Sequence of amino	Adhesin/CTXA2B chi	Sequence of amino	CTP3 epitope of th	Cholera toxin B an	Residues 50-64 of	toxin	Cholera toxin B su	Bovine rotavirus V
20 AAW67443	21 AAY87462	17 AAW04857	17 AAR94939	17 AAW06606	17 AAW06607	19 AAW80808	11 AAR04163	10 AAP93561	17 AAW06605	19 AAW59770			15 AAR50227		12 AAR11272	æ	21 AAY96872		Ø		19 AAW74466	19 AAW80599		6 AAP50436	4 AAP30600	20 AAY32094	4 AAP30265			16 AAR76748	-	21 AAB15525	21 AAB15526
371	21	103	103	103	103	103	118	124	124	124	124	131	138	170	405	103	124	126	41	124	461	749	1338	46	47	461	56	15	15	23	12	, 15	15
100.0	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	94.4	91.6	88.8	88.8	87.9	83.2	83.2	83.2	83.2	82.2	81.8	9.92	74.8	71.0	. 71.0	71.0	57.9	57.0	57.0
107	101	101	101	101	101	101	101	101	101	101	101	101	101	101	101	86	95	95	46	89	89	68	68	88	87.5	82	80	16		97	62	61	61
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27		29		31	32	33	34	35	36	37	38	39	40	41	42	43:	44	45

## ALIGNMENTS

RESULT

Heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea. E. coli heat labile enterotoxin B-derived peptide, SEQ ID NO:5. 21 AA AAY87463 standard; peptide; 03-JUL-2000 (first entry) AAY87463; AAY87463 

Escherichia coli.

WO200014114-A1.

16-MAR-2000

99WO-GB02970. 07-SEP-1999;

98GB-0019484 (UYBR-) UNIV BRISTOL. 07-SEP-1998;

Williams NA, Hirst TR;

WPI; 2000-256943/22.

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor GM-1

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Disclosure; Fig 5; 54pp; English.
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Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                       The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from vibrio cholerae which do not bind to the ubiquitous GM-I ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit CC is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB) actilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-I receptors. Although GM-I binding is responsible for some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated beta-4 - alpha-2 loop of EtxB and/or CtxB, exerting the same effects as cormal EtxB and CtxB subunits, except that they do not bind or cross link can any also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460 being repetively.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 107; DB 21;
Pred. No. 1.4e-11;
Mismatches 0;
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Disclosure; Page 15; 62pp; English
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Read RJ, Stein PE;
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94US-0251121.
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Best Local Similarity 100.
Matches 21; Conservative
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31-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP-ribosylating toxin; PT; crystalline pertussis holotoxin; ETA; DT; three-dimensional structure; LT; immunoprotective; infection.
                                                                                                                                                                                                                                                             Gaps
               ADP-ribosylating toxins, pertussis holotoxtin (PT), E. coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify sites which contribute to PT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella
AAR72540-R72545 are structurally equivalent B-subunits from three
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                                                                                                                                                                                                                    Length 93;
                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                      Score 107; DB 16;
Pred. No. 8.1e-11;
; Mismatches 0;
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                                                                                                                             pertussis infection.
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Oomen RP;
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                                                                                                                                                                93 AA;
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24-AUG-1993;
31-MAY-1994;
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holotoxin, functional (aa) which affect biological properties of the pertussis holotoxin can be identified. This can be used to predict (aa) which contribute to the toxicity of the holotoxin to produce immunoprotective, genetically-detoxified analogues of pertussis holotoxin. The present sequence represents an ADP-ribosylating toxin B-subunit peptide used in the exemplification of the present
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pertussis holotoxin; PT; modified; effector; toxicity; cell binding; enzyme; ADP-ribosylation; toxin; crystalline; X-ray crystallography; structural analysis; interacting site; mitogenicity; adjuvanticity;
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                                                                                                                                                                                                                                                                                                                                                                     Score 107; DB 20;
Pred. No. 8.1e-11;
; Mismatches 0;
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Read RJ, Stein PE;
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94US-0251121
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                                                                                                                                                                                                          invention
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                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Armstrong GD;
                                                                                                                                                                                                                                                                                                                                                                                                Pertussis toxin; heat labile toxin; verotoxin; exotoxin A; holotoxin; diphtheria toxin; ADP-ribosylating toxin; mannose binding protein; infection; crystal structure; X-ray crystallography; detoxification;
                                                                                                                                       Gaps
toxins such as diphtheria toxin (DT), Pseudomonas exotoxin A (ETA), heat-labile toxin of E. coli (LT) and verotoxin-1 (VT). The present sequence represents the beta-subunit of LT toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crystalline form of isolated pertussis holotoxin useful in studying proteins which have functional resemblance -
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                                                                                                         93;
                                                                                                        Length
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                                                                                                         20;
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                                                                                                        Score 107; DB 20;
Pred. No. 8.1e-11;
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                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Heat labile toxin B subunit SEQ ID NO:26.
                                                                                                                                                                                                                                                                          AAY68365 standard; Peptide; 93 AA.
                                                                                                            100.08; Fr. 0;
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                                                                                                         100.08;
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93US-0110947.
94US-0251121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95US-0467976.
                                                                                                                                                                     1 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                     35 getfqvevpgsqhidsgkkai
                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                     21; Conservative
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Oomen RP;
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                                                                                                        Query Match
Best Local Similarity
                                                             93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995;
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31-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunogenic.
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Hazes B,
                                                                                                                                                                                                                                                                                                         AAY68365;
                                                               Sequence
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Exotoxin mucosal cell binding motif; nucleic acid delivery; nucleic acid affinity domain; heat-labile enterotoxin.
                                                                                              Recombinant exotoxin protein variant LTBpL.
   AAB73241 standard; Protein; 134 AA
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                                                              14-MAY-2001 (first entry)
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N-PSDB; AAF75712.
                                                                                                                                                                                                                                                                                                                         (AGRI-) AGRIVAX INC
                                                                                                                                                                                                  WO200111960-A1
                                                                                                                                                                       Unidentified.
                                                                                                                                                                                                                                                                                              18-AUG-1999;
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                                 AAB73241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a method for producing a pertussis toxin (also designated lymphocytosis-promoting factor, histamine-sensitising factor and islet activating protein) with a modified biological activity, involving analysing the crystal structure of the protein to identify active sites which can then be modified. This may lead to an alteration in the toxicity, cell binding or enzyme activity of the toxin. This can be used in the production of immunoprotective analogues of pertussis toxin is the cause of whooping cough following infection
                                                                                                                                                                                                                                                                                         Pertussis toxin; crystal structure; whooping cough; biological activity; lymphocytosis-promoting factor; histamine-sensitising factor; islet-activating protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modifying pertussis holotoxin to produce detoxified PT analogs, comprising analyzing crystalline structure of toxin, to identify sites of toxicity, cell binding or enzyme activity of PT and modifying identified site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klein MH, Armstrong GD;
                                   Gaps
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    Length 93;
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                                 Indels
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100.0%; Pred. No. 8.1e-11;
ive 0; Mismatches 0;
Score 107; DB 21;
Pred. No. 8.1e-11;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loosmore S,
                                                                                                                                                                                                                                                              E coli verotoxin-1 B subunit SEQ ID NO: 26.
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100.0%; Sc
100.0%; Pr
tive 0;
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                                                                                                                                                                      AAB66239 standard; Protein; 93
                                                              1 GETFQVEVPGSQHIDSQKKAI 21
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93US-0110947.
94US-0251121.
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                                                                               (first entry)
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              Best Local Similarity 100.
Matches 21; Conservative
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Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93
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24-AUG-1993;
31-MAY-1994;
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Hazes B,
                                                                                                                                                                                                  AAB66239;
   Query Match
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The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid affinity domain. The present sequence is one such protein variant. In the present invention the heat-labile enterotoxin (LT) of Escherichia coli was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (DARE) family. The protein variants are useful for selectively delivering nucleic acid to mucosal cells, for inducing an immune response when the nucleic acid encodes an antigen to which the immune response is desired, for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein in a subject, by administering a composition
Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding motif of an exotoxin and a nucleic acid affinity domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 107; DB 22; 100.0%; Pred. No. 1.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant exotoxin protein variant LTBpLh.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                          Example 1; Fig 9; 57pp; English.
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Matches 21; Conserv
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Gaps

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Indels

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RESULT

1 GETFQVEVPGSQHIDSQKKAI 21

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21; Conservative

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The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid affinity domain. The present sequence is one such protein variant. In the present invention the heat-lable enterotoxin (LT) of Escherichia coli was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (DARE) family. The protein variants are useful for selectively delivering nucleic acid to mucosal cells, for inducing an immune response when the nucleic acid encodes an antigen to which the immune response is desired, for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein variant.
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                                                                                           Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding motif an exotoxin and a nucleic acid affinity domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 107; DB 22;
100.0%; Pred. No. 1.5e-10;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                       Example 1; Fig 11; 57pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Watches 21; Conservative
WPI; 2001-211103/21.
N-PSDB; AAF75714.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAF75715.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 107; DB 22;
Pred. No. 1.3e-10;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant exotoxin protein variant LTB-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB73243 standard; Protein; 155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig 10; 57pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 21; Conservative 0;
                                                                                                                                                                                                                       99US-0149294.
                                                                                                                                                         18-AUG-2000; 2000WO-US22715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-AUG-2000; 2000WO-US22715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            990S-0149294
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                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-211103/21.
N-PSDB; AAF75713.
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                                                                                                                                                                                                                                                                                  (AGRI-) AGRIVAX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 AA;
                             WO200111960-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200111960-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                       18-AUG-1999;
                                                                                           22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Welter LM;
                                                                                                                                                                                                                                                                                                                                             Welter LM;
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AAB73243 RESULT

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was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (bARE) family. The protein variants are useful for selectively delivering nucleic acid to mucosal cells, for inducing an immune response when the nucleic acid encodes an antigen to which the immune response is desired, for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein in a subject, by administering a composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion protein; labile toxin B subunit; LT-B; E. coli; flagellin; flaA; C. jejuni; antigenic; colonisation; chicken; Campylobacter; vaccine; immune response; ganglioside GM1; immunoglobulin A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant fusion gene expressing Campylobacter jejuni flagellin
                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                     Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Labile toxin (LT-B)/flagellin (flaA) fusion protein.
                                                                                                                                                                                                                                                                                                                                                               Score 107; DB 22;
Pred. No. 1.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Column 16-20; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY01300 standard; Protein; 371 AA
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                     the protein variant
                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-0150305,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97US-0784218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USDA ) US SEC OF AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Campylobacter jejuni.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-243214/20.
                                                                                                                                                                                                                                                               163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX27771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5888810-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAR-1999.
                                                                                                                                                                                                     comprising
                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY01300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY01300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a recombinant fusion protein consisting of the Campylobacter jejuni flagellin protein (flaA) fused to the Escherichia coli B subunit of the labile toxin (LT-B). The fusion protein is antigenic and when administered in vaccines decreases colonisation of chickens by Campylobacter species. The LT-B component serves to deliver the flagellin antigen to mucosal surfaces and also has an adjuvant effect
                                                                                                                                                                                                                                                                 Recombinant; fusion protein; flagellin; flaa; labile toxin; antigen; vaccine; colonisation; chicken; mucosal surface; adjuvant; secretion; immunoglobulin A.
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant fusion protein of Campylobacter jejuni flagellin protein and Escherichia coli labile toxin – useful in vaccines to reduce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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 Length 371;
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                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Escherichia coli labile toxin – useful in vac
colonisation of chickens by Campylobacter species
100.0%; Score 107; DB 20;
100.0%; Pred. No. 4.2e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 107; DB 20;
100.0%; Pred. No. 4.2e-10;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                        C. jejuni flagellin/E. coli LT-B fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Column 17-20; 14pp; English.
                                                                                                                                                         AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY87462 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                            Chimeric - Campylobacter jejuni.
Chimeric - Escherichia coli.
                                                                                                                                                      AAW67443 standard; Protein; 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         on immunoglobulin A secretion.
                                                       21
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                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0829026.
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97US-0829026.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Meinersmann RJ;
                                                                      49 getfqvevpgsqhidsqkkai
                                                       1 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GETFOVEVPGSOHIDSOKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 getfqvevpgsqhidsqkkai
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USDA ) US SEC OF AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-023536/02.
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Best Local Similarity
Matches 21; Conserv
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV34380.
                                                                                                                                                                                                                                                                                                                                                                                                                             31-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1997;
                                                                                                                                                                                                              02-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                      US5837825-A.
                Best Local Sim
Matches 21;
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                                                                                                                                                                                  AAW67443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
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ID AAY8
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cough; recombinant construct;

(first entry)

Zealey GR;

Yacoob RK,

Loosmore SM,

96WO-CA00107 95US-039334

us-09-786-648-5.rag

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Recombinant constructs for expressing and opt. secreting proteins in Bordetella - comprise Bordetella promoter coupled to non-Bordetella, esp. cholera B toxin, gene or coupled to non-Bordetella leader and
                                                                                                                                                       structural protein; receptor; heterologous gene; leader; promoter.
                                                                                                          cholera toxin B subunit; enzyme; antigen; immunogen; allergen; enzyme inhibitor; hormone; lymphokine; immunoglobulin; toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Figure 1; 61pp; English.
                                               Synthetic cholera toxin B subunit.
                                                                                          Bordetella pertussis; whooping
                                                                                                                                                                                                                                                                                                                                                                                                                   (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-425088/42.
N-PSDB; AAT38038.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene of interest
                                                                                                                                                                                                                                                                                                                               23-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                        23-FEB-1995;
  21-FEB-1997
                                                                                                                                                                                                                                         WO9626282-A1
                                                                                                                                                                                                                                                                                    29-AUG-1996.
                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein MH,
    The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera coxin (Citx) from Vibrio cholerae which do not bind to the ubiquitous GM-1 ganglioside receptors on host cell surfaces. Both Etx and ctx and ctx and composed of one A subunit and five identical B subunits. The A subunit composed of one A subunit while the B subunits. The A subunit cross-linking of GM-1 receptors. Although GM-1 binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated control of GM-1 properties of the invention are fragments of the beta-4 - alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and ctxB subunits, except that they do not bind or cross link GM-1. They may be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460 being repersent preferred.
                                                                                                                            Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor \mathsf{GM-1} .
                                                                                 Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 101; DB 21;
Pred. No. 1.5e-10;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 15; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 94.4%;
Best Local Similarity 95.2%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                        99WO-GB02970
                                                                                                                                                                                                                                                                                                                                                                                                                 98GB-0019484
                                           03-JUL-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Williams NA, Hirst TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYBR-) UNIV BRISTOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-256943/22.
                                                                                                                                                                                                                  Vibrio cholerae.
Escherichia coli.
                                                                                                                                                                                                                                                                               WO200014114-A1.
                                                                                                                                                                                                                                                                                                                                                                     07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                              07-SEP-1998;
                                                                                                                                                                                                                                                                                                                             16-MAR-2000
AAY87462;
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Recombinant constructs comprising a promoter functional in Bordetella leader sequence for a heterologous gene or a non-construct la leader sequence for secretion of a gene product which may or may not be of Bordetella, immunogens, allergens, enzymes or may not be of Bordetella, immunogens, allergens, enzyme in Bordetella of enzymes, antigens, immunoglobulins or their fragments, toxins, mammalian proteins, structural proteins or receptors. The Bordetella strains are particularly engineered to express the cholera toxin B subunit (this sequence). The promoters used in the constructs are selected from the Bordetella pertussis tox, fha promoters or the high molecular weight (hmw) outer membrane promoter of non typable Haemophilus influenzae; leaders used in the constructs are selected from the cholera toxin B leader (CTB-L), the pertussis toxin subunit s1 leader (S1-L) and the pertussin pertactin leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a leader (CTB-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the constructs are selected from a leader (PRN-L); and genes used in the leader (PRN-L); and genes used in the constructs are selected from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.4%; Score 101; DB 17;
95.2%; Pred. No. 9.7e-10;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heat labile enterotoxin B subunit (LT-B) E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR94939 standard; Protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-OCT-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Sin
Matches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR94939;
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AAR94939
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Gaps

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Indels

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AAW04857 standard; Protein; 103 AA.

RESULT 14

AAW04857;

substitution

/label=

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17
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ÷
                                                                                                                                                                                                                                                                  A transgenic plant comprising or expressing a DNA sequence encoding an immunogenic agent can be be used as an oral vaccine for animals. The vaccine is administered by the oral consumption of the plant and provides the first known functional method for immunising animals using transgenic plants, where the plants express bacterial antigens that act as both immunogens and adjuvants. The method provides an inexpensive production and delivery system for such antigens to animals. This is the LT-B Escherichia coli toxin subunit and its coding sequence was used in the construction of such a transgenic plant. The immunogenic agent preferably comprises the LT-B or CT-B (cholera toxin B.subunit) or optionally LT-A or CT-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; CTB; heat labile enterotoxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea; vonniting; food poisoning.
                                                                                                                                                                                                                  Transgenic plants contg. E. coli heat labile enterotoxin subunits used as oral vaccines for animals which consume the plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                              .
0
 Toxin; subunit; vaccine; transgenic plant; immunogen; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 101; DB 17; Length 103;
Pred. No. 9.7e-10;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= substitution
/note= "wild-type Thr replaced by Ala"
Misc-difference 94
                                                                                                                                                                  Mason HS;

    Vibrio cholerae.
    Enterotoxigenic Escherichia Coli.

                                                                                                                                                                                                                                                 Disclosure; Page 100-101; 130pp; English.
                                                                                                                                                                 Clements JD, Hag TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW06606 standard; Protein; 103 AA.
                                                                                                                                   (TULA ) TULANE EDUCATIONAL FUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45 gatfqvevpgsqhidsqkkai 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21
                                                                                                                                                                                                                                                                                                                                                                                                                         94.48;
95.28;
                                                                                           95WO-US13376
                                                                                                              94US-0328716
                                                                                                                                                                                  WPI; 1996-230602/23.
N-PSDB; AAT18799, AAT18800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.2
Matches 20; Conservative
         adjuvant; immunisation
                                                                                                                                                                                                                                                                                                                                                                                             AA;
                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                           103
                                                  WO9612801-A1
                                                                                          24-OCT-1995;
                                                                                                              24-OCT-1994;
                                                                                                                                                                 Arntzen CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1997
                                                                      02-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW06606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
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AAW06606
ID AAW0
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AAW06606 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding aa from heat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea cand vomiting, in humans and animals.

Note - This sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; CTB; heat labile enterotoxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea; vomiting; food poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sub-unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
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/note= "wild-type His replaced by Asn"
                                                       /label= substitution
/note= "wild-type Ala replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 101; DB 17;
Pred. No. 9.7e-10;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric – Vibrio cholerae.
Chimeric – Enterotoxigenic Escherichia Coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW06607 standard; Protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 3; Page -; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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95.2%;
                                                                                                                                                                                                                                                                         96WO-SE00570.
                                                                                                                                                                                                                                                                                                                                   95SE-0001682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GETFQVEVPGSQHIDSQKKAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holmgren J, Lebens MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-506108/50.
                                                                                                                                                                                                                                                                                                                                                                                           (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT43576
                                 Misc-difference
                                                                                                                                                                                                                                                                         02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                   05-MAY-1995;
                                                                                                                                                WO9634893-A1
                                                                                                                                                                                                              07-NOV-1996
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RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                         AAW06607 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic lilness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                               and vomiting, in humans and animals.

Note - This sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                                               Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Key Location/Qualifiers
Misc-difference 1..25
/label= substitution
/note= "the first 25 amino acids of mature
wild-type cholera toxin B subunit are
replaced with the first 25 amino acids
of mature enterotoxin B subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of the wild type chorela toxin B subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 101; DB 17;
Pred. No. 9.7e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW80808 standard; protein; 103 AA.
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                                                                                                                                                                                                                                                                                         Claim 4; Page -; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 gatfqvevpgsghidsgkkai 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94.4%;
                                                                                                                         96WO-SE00570
                                                                                                                                             95SE-0001682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                               Holmgren J, Lebens MR;
                                                                                                                                                                                                                  WPI; 1996-506108/50.
                                                                                                                                                                 (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 AA;
                                                                                                                                                                                                                              N-PSDB; AAT43577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9845324-A1
                                                                                  WO9634893-A1
                                                                                                                        02-MAY-1996;
                                                                                                                                             05-MAY-1995;
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                                                                                                     07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW06605).
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cholera toxin B-subunit; hybrid protein; heterologous IgA active antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                             New mutant cholera toxin selected from a group comprising nontoxic subunits/derivatives - effective as an adjuvant when coadministered with an antigen to birds and mammals
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/*label= signal peptide
/*note= absent from mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 101; DB 19;
Pred. No. 9.7e-10;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                Yamamoto
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/*label= His or Tyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 1B; 43pp; English.
                                                                                                                                                                                                                                                                             Takeda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      administered subcutaneously
                                             98WO-US06725
                                                                                         97US-0043410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89WO-0000495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GETFQVEVPGSQHIDSQKKAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cholera Toxin B-subunit.
                                                                                                                                  (KIYO/) KIYONO H.
(MCGH/) MCGHEE J R.
(TAKE/) TAKEDA Y.
(UABR-) UAB RES FOUND.
(TAMA/) YAMAMOTO S.
                                                                                                                                                                                                                                                                             Kiyono H, Mcghee JR,
                                                                                                                                                                                                                                                                                                                         WPI; 1998-594478/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
misc_difference
                                             03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-1989;
                                                                                         04-APR-1997;
15-0CT-1998.
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L'Hoir C,

Sequence

Query Match

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In the patent, the DNA encoding LT-B is expressed as part of a fusion protein with an epitope of a malaria parasite, eg Region I or Region II or repeat region of circumsporozoite protein antigen (CS) (AAP93560) from Plasmodium berghei. Pref. the fusion gene is inserted into attenuated Salmonella enteriditis under the left promoter control of lambda. Such bacteria can multiply in the host without causing disease or disorder and express CS that will induce a protective immune response against malaria and can be used in vaccines. Such vaccines can be multivalent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cholera toxin B subunit, used for hybrid immunogenic toxin production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW06605 is the full (including the signal peptide) length cholera toxin B subunit (CTB), this sequence is described as unpublished in the specification. The mature CTB protein was used to create hybrid mutants, in which certain amino acids (aa) of CTB were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB), see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; heat labile enterotoxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea; vomiting; food poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                                                                                               Length 124;
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                           Score 101; DB 10;
Pred. No. 1.2e-09;
); Mismatches 1;
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/label= sig_peptide
22..124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22..124
/label= mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW06605 standard; Protein; 124 AA.
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                                                                                                                                                                                                                                                                                                                                                                     86
                                                                                                                                                                                                                                                               94.4%;
95.2%;
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                                                                                                                                                                                                                                                                                                                                 GETFQVEVPGSQHIDSQKKAI
| ||||||||||||||||||||||||||||||gatfqvevpgsqhidsqkkai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holmgren J, Lebens MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-506108/50.
N-PSDB; AAT43575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HOLM/) HOLMGREN J. (LEBE/) LEBENS M R.
                                                                                                                                                                                                           124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9634893-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAY-1995;
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                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW06605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 21
                                                                                                                                                                                                                                                                                                                                     Н
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         *888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                            Mature cholera toxin B-subunit is obtained when the signal peptide is cleaved off. There is an Ochre codon at position 343-5; the sequence downstream from it is part of a plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B subunit of the heat-labile enterotoxin (LT-B) derived from E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B subunit; heat-labile enterotoxin; LT-B; Escherichia coli; malaricircumsporozoite protein; fusion protein; live recombinant vaccine; Salmonella; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                 New hybrid protein, useful in vaccines \boldsymbol{\cdot} contains cholera toxin b subunit and heterologous IgA active
                                                                                                                                                                                                                                                                                                                                                                                                         Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Live recombinant vaccine for malaria -
comprising attenuated entero-invasive bacterium contg. DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      94.4%; Score 101; DB 11;
95.2%; Pred. No. 1.1e-09;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pillai S, Hockmeyer WT;
                                       (UYLI-) L'UNIVERSITE DE L'ETAT A LIEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1..22
/note="Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding epitope of malaria parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23..124
/note="Mature LT-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP93561 standard; protein; 124 AA.
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                                                                              Martial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                          Disclosure; ; pp; French.
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                                                                              Renard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1989-114399/15.
N-PSDB; AAN90747.
                                                                                                              WPI; 1990-132273/17
                                                                                                                                                                                                         antigenic sequence.
                                                                                                                                                                                                                                                                                                                                                  118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                 N-NSDB; 004046
     27-SEP-1988;
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AAP93561;

RESULT AAP93561

Peptide Protein

95.28;

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AAW06606 and AAW06607. The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the amino acid sequence of Escherichia coli beta-subunit of heat labile enteritoxin (LTB). It is used in the method of the invention to create fusion proteins which are useful as vaccinating immunogens. The fusion proteins are useful in vaccines, specifically where the antigenic peptide is an inhibin fragment for increasing the fertility of an animal (by increasing levels of follicle stimulating hormone (FSH) or production of sperm or ova), but more generally for inducing an immune response against the antigenic peptide. Vaccines are particularly administered orally, e.g. fusion protein is expressed in edible plants or animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Beta-subunit of heat labile enterotoxin; LTB; fusion protein; vaccine; immunogen; antigen; inhibin; fertility; follicle stimulating hormone;
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding fusion of antigenic peptide and enterotoxin sub-unit - useful as vaccinating immunogen, particularly for increasing animal fertility by inducing antibodies against
                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                      94.4%; Score 101; DB 17; Length 124; 95.2%; Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of E. coli LTB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bagdasarian M, Ireland J;
                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 95.2 les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-297947/26.
N-PSDB; AAV41573.
                                                                                                                                                                                                                                                 124 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli,
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                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches
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Length 124;

DB 19;

94.4%; Score 101;

Query Match

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This synthetic Escherichia coli heat-labile toxin (LT) B subunit (LT-B) is encoded by a plant-codon optimized cDNA. The cDNA sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. The second codon is changed from AAT encoding year to GTG encoding Val, in order to create a Ncol restriction site at the 5' end. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the polynucleotides are useful for the transformation of plant cells for the prophylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are
                              ö
                                                                                                                                                                                                                                                                                   Heat-labile toxin; LT-A; LT-B; mutant; transgenic plant; vaccine; oral; adjuvant; anti-bacterial.
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic compositions to elicit immune responses in animals
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                              Indels
                                                                                                                                                                                                                                                              Plant-optimized E. coli heat labile toxin B subunit.
Pred. No. 1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                         22..124
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                        /label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BOYC-) BOYCE THOMPSON INST PLANT RES. (MASO/) MASON H S. (ARNI/) ARNIZEN C J.
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                   AAY96652 standard; Protein; 124 AA.
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                                                                       66 gatfqvevpgsqhidsqkkai
                                                            1 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           also useful as adjuvants.
            Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mason HS, Arntzen CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-442653/38.
                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                    AAY96652;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
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Gaps

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Indels

Length 131;

Score 101; DB 11; Pred. No. 1.3e-09; Mismatches

94.4%; 95.2%;

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21

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This allows the use of a strategically placed EcoRI site just upstream
        of the RBS on the LTB gene for the insertion of a strong tac promoter for the expression of CTB. The protein can be used as Vaccines, diagnostic reagents and receptor-blocking agents for prophylaxis of cholera and E.coli diarrhoea.
                                                                                                                        GETFQVEVPGSQHIDSQKKAI
                                                                                               Conservative
                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                                            31-MAR-1994.
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                                                                                                                                                                                                                                                                                           WO9406465-A
                                                                                              20;
                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                            AAR50227;
                                                    Sequence
                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                 Dale JB;
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                                                                                                                                 73
                                                                                               Matches
                                                                                                                                                            RESULT
888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expression of binding sub-unit protein of cholera toxin - using foreign promoter with no V cholera DNA between promoter and ribosome binding site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is produced by genetically fusing the leader sequence for E.coli heat-labile enterotoxin subunit (LTB) by its 3' SacI end to the 5' NdeI end of the cholera toxin subunit (CTB) via a synthetc linker.
                  Gaps
                 ö
Score 101; DB 21; Length 124; Pred. No. 1.2e-09;
                 Indels
                                                                                                                                                                                                                                                                                                   24..25
/label-cleavage to release mature CTB
                                                                                                                                                                                                                                                                                                                             CIB
                                                                                                                                                                                                                                                                  25..28
/label=part of CTB leader sequence
                                                                                                                                                                                                                                                                                                                                                                                                 Tabel = D = N in classical 569B CTB
                                                                                                                                                                                                                                                                                                                                                                                                                  = N in classical 569 CTB
                                                                                                                                                                                                                                       'label=first AA of mature LTB
                                                                                                                                                                                                                                                23..24
/label-AAs encoded by linker
      Pred. No. 1.26
); Mismatches
                                                                                                                                                                                                               1..21
/label=LTB leader sequence
                                                                                                                                                                                                                                                                                                                                                                Tor CTB
                                                                                                                                                                                                                                                                                                                                              Tor CTB
                                                                                                                                                                                                                                                                                                                                                                                Tor CTB
                                                                                                                                                                    Cholera toxin; diarrhoea; enterotoxin.
                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                     5..26
label=cleavage to
                                                                                              AAR04825 standard; protein; 131 AA.
                                                                                                                                                                                                                                                                                                                                             label-H - Y in El
                                                                                                                                                                                                                                                                                                                                                               label-T = I in El
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                                                                                                                                                                                                                                                                                           'label-mature CTB
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0
94.48;
                                 1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                    Vibrio cholreae serogroup 01
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                                           (first entry)
                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  /label=D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; ; p; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΰ
                                                                                                                                                 LTB-CTB fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sanches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1990-149724/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HOLM/) HOLMGREN J.
        Local Similarity
                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAR04825
                                                                                                                                                                                                                                                                                                                                                      Misc-difference
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15-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-1989;
                                                                                                                                 25-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holmgren J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                    EP368819-A,
                                                                                                               AAR04825;
Query Match
                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                               Peptide
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         Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant hybrid streptococcal M protein antigen(s) - which elicit opsonic antibodies without eliciting cross-reactive antibodies to mammalian heart tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                   B subunit; labile toxin; M protein; fusion protein; antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Group A streptococci; rheumatic fever; pharyngitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 101; DB 15;
Pred. No. 1.4e-09;
); Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                       Sequence of LT-B-M24 hybrid molecule.
                                                                                                                                                                       ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYTE-) UNIV TENNESSEE RES CORP.
                                                                                                                                                                AAR50227 standard; Protein; 138
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93
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95.2%;
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Mon Jul 16 16:58:12 2001

Qy Dp

Search completed: July 16, 2001, 16:35:42 Job time: 206 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

July 16, 2001, 16:32:16 ; Search time 56.06 Seconds (without alignments) 7.570 Million cell updates/sec

Title:

US-09-786-648-2 39 1 EVPGSQH 7 Perfect score: Sedneuce:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

412676 Total number of hits satisfying chosen parameters: 412676 seqs, 60623988 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/Aa1997.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/Aa1998.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1999 DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA2000.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT: /SIDSB/gcgdata/geneseq/geneseqp/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	Cholera toxin B/en	Cholera toxin B/en	Cholera toxin B/en	CTP3 epitope of th	Cholera toxin B an	Cholera toxin B/en	E. coli heat labil	Residues 50-64 of	Sequence of amino	Network polymer wh	Network polymer wh
		Ω	AAY87460	AAY87464	AAY87461	AAP93498	AAR85125	AAY87462	AAY87463	AAR76748	AAP30265	AAP50439	AAP50436
		DB.	21	21	21	10	16	21	21	16	4	9	9
	Query	Length	7	œ	12	15	15	21	21	23	26	41	46
þ	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
		Score	39	38	39	39	39	39	39	39	39	39	39
	Result	No.	-	7	ĸ	4	'n	9	7	ω	σ	10	11

Sequence of amino	ADP-ribosylating t	Escherichia coli v	E. coli heat-labil	Heat labile toxin	E coli verotoxin-1	Sequence of sub-un	Synthetic cholera	Heat labile entero	Cholera toxin B su	Cholera toxin B su	. Amino acid sequenc	Cholera Toxin B-su	B subunit of the h	Cholera toxin B su	Amino acid sequenc	Plant-optimized E.	Plant-optimized V.	GtfB.1/CTB chimeri	LTB-CTB fusion pro	Recombinant exotox	Sequence of LT-B-M	Recombinant exotox	Recombinant exotox	Recombinant exotox	LTB-CTP fusion pro	Labile toxin (LT-B	C. jejuni flagelli	HSV-1 antigen/heat	Human secreted pro	B subunit of CT.	Human secreted pro	Human heart lecith	Murine lecithin-ch
AAP30600	AAR72545	AAY41816	AAW95226	AAY68365	AAB66239	AAP50340	AAW04857	AAR94939	AAW06606	AAW06607	AAW80808	AAR04163	AAP93561	AAW06605	AAW59770	AAY96652	AAY96872	AAR12630	AAR04825	AAB73241	AAR50227	AAB73242	AAB73243	AAB73244	AAW94082	AAY01300	AAW67443	<b>AAR1127</b>	# AAG02635	AAR28831		AAW8093	AAW80939
4	16	20	20	21	22	9	17	17	17	17	19	11	10	17	19	21	21	12	1	22	15	22	22	22	50	20	50	12,	213	13	21	19	13
47	93	93	93	93	93	103	103	103	103	103	103	118	124	124	124	124	124	126	131	134	138	142	155	163	170	. 371	. 371	405	51	124	318	379	379
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	87.2	84.6	84.6	84.6	84.6
39	39	39	39	36	39	39	39	39	39	39	39	39	39	39	39	39	33	33	39	39	39	39	36	39	39	39	39	39	34	33	33	33	33
12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT AAY87460

AAY87460 standard; peptide; 7 AA.

AAY87460;

03-JUL-2000 (first entry)

Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:2.

Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea. 

Escherichia coli. Vibrio cholerae.

WO200014114-A1.

16-MAR-2000.

99WO-GB02970 07-SEP-1999; 98GB-0019484. 07-SEP-1998;

(UYBR-) UNIV BRISTOL.

Hirst TR;

Williams NA,

WPI; 2000-256943/22.

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor GM-1

The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholers toxin (Ctx) from vibil cholerae which do not bind to the ubiquitous CM-1 ganglioside receptors on host cell surfaces. Both Etx and ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, while the B subunits (EtxB and CtxB) ribosyltransferase activity, while the B subunits (EtxB and CtxB) across-linking of GM-1 receptors. Although GM-1 binding is responsible. Cor some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding; The peptides of the invention are fragments of the beta-4- alpha-2 loop of EtxB and CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced disarnhoea. Sequences AAY87460-Y87463 Claim 1; Page 13; 62pp; English. 

Sequence

Gaps ö 100.0%; Score 39; DB 21; Length 7; 100.0%; Pred. No. 3.4e+05; ive 0; Mismatches 0; Indels Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative

g å

AAY87464 standard; peptide; 8 AA.

AAY87464;

(first entry) 03-JUL-2000

Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.

Cholera toxin B/enterotoxin B-derived immunomodulatory peptide.

Vibrio cholerae. Escherichia coli.

WO200014114-A1.

99WO-GB02970. 07-SEP-1999; 16-MAR-2000

98GB-0019484 07-SEP-1998;

(UYBR-) UNIV BRISTOL.

Williams NA, Hirst TR;

WPI; 2000-256943/22.

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor  $\mathsf{GM-1}$ AAY87464

XX
AC AAY87

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DE Chol.
XX
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Example 5; Page 45; 62pp; English.

The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera coxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous CG M-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit ciposyltransferase activity, while the B subunits (EtxB and CtxB) ADP-cribosyltransferase activity, while the bost cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible CC cross-linking of GM-1 receptors. Although GM-1 binding is responsible corps-linking of GM-1 receptors. Although GM-1 binding is responsible corps-linking of GM-1 as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention (AAVG7461-Y87463) are crasments of the beta-4-alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal ExxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an inhibitor for immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the composition for treating, preventing and/or modulating a corresponding to a portion of the beta-4-alpha-2 loop of EtxB and CtxB corresponding to a portion of the beta-4-alpha-2 loop of EtxB and CtxB corresponding to a portion of the beta-4-alpha-2 loop of EtxB and CtxB carnes immunomodulatory effects. Peptide AAVG7464 corresponds to residues corresponding to a portion of the beta-4-alpha-2 loop of EtxB and CtxB carnesponding to a portion of the beta-4-alpha-2 loop of EtxB and CtxB candomly selected control peptide. 

¥ Seguence

Gaps .; 0 Length 8; Indels 100.0%; Score 39; DB 21; 100.0%; Pred. No. 3.4e+05; cive 0; Mismatches 0; Conservative Query Match Best Local Similarity '... 7; Conserv?

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1 evpgsqh 7 EVPGSQH 7 q à

AAY87461 RESULT

AAY87461 standard; peptide; 12 AA

AAY87461;

03-JUL-2000 (first entry)

Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:3.

Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.

Escherichia coli. Vibrio cholerae

WO200014114-A1.

16-MAR-2000.

99WO-GB02970. 98GB-0019484. 07-SEP-1999; 07-SEP-1998;

(UYBR-) UNIV BRISTOL. 

Williams NA,

WPI; 2000-256943/22.

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor  $\mathsf{GM-1}$ 

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RESULT
AAR85125
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                                                                                                                                                                                                                                                         g
                                          The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubjusticous GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB).

Thosyltransferase activity, while the B subunits (EtxB and CtxB) accilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain through GM-1 binding is responsible.

Through GM-1 binding The peptides of the invention are fragments of the chrough GM-1 binding The peptides of the invention are fragments of the beta-4 alpha-2 loop of EtxB and/or CtxB. exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 represent preferred peptides of the invention, AAX87460 being
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant flagellin gene including sequence - for heterologous epitope, and expressed fusion proteins, useful in vaccines and for prodn. of antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epitope of Cholera toxin B subunit; flagellin fusion protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39; DB 21; Length 12; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTP3 epitope of the Cholera toxin B subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Preu, ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stocker BAD, Newton SMC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (STRD ) LEYLAND STANDFORD JUNIOR UNIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; fig.4B; 137pp; English.
               Disclosure; Page 15; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP93498 standard; protein; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PRAX-) PRAXIS BIOLOGICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89WO-US01932
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccine; immunotherapy; ds;
                                                                                                                                                                                                                                                                                                                                                                                                                               particularly preferred
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N-PSDB; AAN92414.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAY-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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à g This sequence corresponds to the CTP3 epitope of the Cholera toxin B

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                                                                                                                                                                                                                                   Gaps
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subunit. The DNA sequence encoding this ligates to othersynthetic oligonucleotides to form a new recombinant gene. This encodes a flagellin fusion protein which can be used in vaccines for immuno-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A compsn. comprising a conjugate of an antigenic cholera B toxin peptide fragment (e.g. AAR85126-30 and esp. AAR85125), covalently bound to a microparticulate inert carrier (e.g. modified silica or thyroglobulin) can be used as an oral vaccine for immunisation against cholera infection. The inert carrier is insoluble in the digestive tract, allowing presentation of the antigen in the intestines, where it will elicit antibodles mainly of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccines for oral immunisation against infecting agents, e.g. cholera - comprise a conjugate of an antigen of an infecting agent covalently bound to micro:particulate inert carrier, e.g. modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conjugate; cholera; B toxin; peptide fragment; microparticulate; inert carrier; modified silica; thyroglobulin; oral vaccine; immunisation; infection; insoluble; digestive tract; antigen; intestines; antibodies; secretory; IgA class.
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                                                                                                                                                                                     Length 15;
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                                                                                                                                                                                 100.0%; Score 39; DB 10;
100.0%; Pred. No. 0.2;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 39; DB 16; 100.0%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cholera toxin B antigenic peptide fragment CTP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR85125 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; Page 25; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sela M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (YEDA ). YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94IL-0109519.
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                                                                                                                                                           Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-403805/51.
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                                                                                                                 A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aldehyde silica
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2 evpgsqh 8
                                                                                                                                                                                                                                                                             1 EVPGSQH 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09529701-A1
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                                                                                                                 Sequence
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                                                                      therapy.
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2 evpgsqh 8

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Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                     Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor \mathsf{GM}\text{-}1
                                                                    Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                        Disclosure; Page 15; 62pp; English.
                AAY87462 standard; peptide; 21 AA.
                                                                                                                                                                                                   98GB-0019484
                                                   (first entry)
                                                                                                                                                                                                                                     Hirst TR;
                                                                                                                                                                                                                    (UYBR-) UNIV BRISTOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
'-had 7; Conserva
                                                                                                                                                                                                                                                     WPI; 2000-256943/22.
                                                                                                                      Vibrio cholerae.
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 AA;
                                                                                                                                                 WO200014114-A1.
                                                                                                                                                                                  07-SEP-1999;
                                                                                                                                                                                                   07-SEP-1998;
                                                                                                                                                                                                                                    Williams NA,
                                                   03-JUL-2000
                                                                                                                                                                 16-MAR-2000.
                                 AAY87462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
9
RESULT
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Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the  ${\rm glycolipid}$  receptor GM-1 -

Disclosure; Page 15; 62pp; English.

Heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.

Escherichia coli.

WO200014114-A1.

99WO-GB02970. 98GB-0019484.

07-SEP-1999; 07-SEP-1998;

16-MAR-2000

Williams NA, Hirst TR; (UYBR-) UNIV BRISTOL.

WPI; 2000-256943/22.

É. coli heat labile enterotoxin B-derived peptide, SEQ ID NO:5.

03-JUL-2000 (first entry)

AAY87463;

AAY87463 standard; peptide; 21 AA.

AAY87463

RESULT

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The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera conflicts from Vibrio cholerae which do not bind to the ubdiquitous GM-1 gangiloside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, while the B subunits (EtxB and CtxB) ribosyltransferase activity, while the B subunits (EtxB and CtxB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the beta-4 alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and ctxB subunits, except that they do not bind or cross link GM-1 They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition of contrating, preventing and/or modulating a disease associated with an immunomedisorder and/or toxin-induced diarrhoea. Sequences AAR87460-Y87463 represent preferred.
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The invention relates to peptide fragments of the Escherichia coll heat labile enterotoxin (Etx) and its closely related homologue, cholera to total from vibrio cholerae which do not bind to the ubdiguitous composed of nom A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB) actilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx. it has been found that certain effects of the toxins, such as immunomodulation, are not mediated for some of the toxins, such as immunomodulation, are not mediated beta-4- alpha-2 loop of EtxB and/or CtxB. exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea Therefore, the peptides may be used in the production of a composition of the creating repersent preferred peptides of the invention. AAY87460 being repersent preferred.
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Best Local Similarity 100.
Matches 7; Conservative
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RESULT AAR76748

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Gaps ö

100.0%; Score 39; DB 21; Length 21; 100.0%; Pred. No. 0.28; Live 0; Mismatches 0; Indels

Conservative

EVPGSQH 7

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6 evpgsqh 12
                                       RESULT
AAP30265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is encoded by a fragment of the the plasmid pLPA93
which was used in the production of fimH fusion genes comprising
the cholera toxin B subunit inserted into the fimH gene. This insert
shows the inclusion of the B subunit into the FimH protein at position
224-226. The chimeric genes were then opt. further modified by insertion
of the hepatitis B virus surface antigen pre-$2 region into a different
position of the FimH adhesin of type I fimbriae. Restriction site handles
(BGIII sites) were introduced into the fimH gene, and the foreign
con insertion of the epitopes did not significantly alter the adhesive
function of the pinches ind not significantly alter the adhesive
con the surface of fimbriae on bacterial hosts illustrated the possibility
con the surface of fimbriae on bacterial presenters of foreign antigens and
continued by the spitopes are as general presenters of foreign antigens and
continued by the spitopes are all the production of variant
continued by the spitopes of the compounds and military of the compounds
continued by the spitopes are all the production of variant
continued by the spitopes are all the production of variant
continued by the spitopes are all the compounds
continued by the spitopes are all the spitopes and miscrobial cells to locations comprising selected receptors to which
                                                                                                     FimH; type 1 fimbriae; organelle; adhesin; alpha-D-mannoside residue; FimA; FimF; FimG; receptor binding site; PCR; amplify; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor specific bacterial adhesins - useful for targetting active compounds and microbial cells to locations of receptors
                                                                           Residues 50-64 of cholera toxin B subunit and FimH 224-226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sokurenko EV;
                                                                                                                                                                                                                                                              "Cholera toxin B subunit 50-64"
                                                                                                                                                                                                            /note= "Represents FimH residue 224"
                                                                                                                                                                                                                                                                                                                   /note= "Represents FimH residue 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pallesen L,
                                                                                                                                                                                                                                    'note= "Linker peptide"
                                                                                                                                                                                                                                                                                       "Linker peptide"
                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 58; 152pp; English.
 AA.
AAR76748 standard; Protein; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molin S,
                                                                                                                                           Chimeric - Vibrio cholerae.
Chimeric - Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                 95WO-DK00042
                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0187166
                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GXBI-) GX BIOSYSTEMS AS.
                                                                                                                                                                                                                                                               /note=
20..22
                                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klemm P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1995-275442/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the adhesins bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 AA;
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N-PSDB; AAQ93061
                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                             WO9520657-A1
                                                                                                                                                                                                                                                                                                                                                                                               27-JAN-1995;
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                                                  18-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hasty DL,
                        AAR76748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                   Peptide
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The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coll (enterotoxin IT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Network polymer which comprises a series of composite E. coli heat-labile toxin (LT)/heat-stable toxin (ST) polypeptide repeating untis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                    Sequence of amino acids 50-75 of the cholera toxin B1 subunit which carries an Arg at posns. 67 and 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
                                                                                                                                                                                                                                       Cholera vaccine; therapy; E.coli infection; enterotoxin LT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dodin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rivaille P, Siffert O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP50439 standard; protein; 41 AA.
AAP30265 standard; Protein; 26 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 11; 13pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a vaccine 1-10mg of active cpd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CNRS ) CNRS CENT NAT RECH SCI (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82FR-0009167.
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                                                                                                        21-APR-1992 (first entry)
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V, Delmas A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1983-834645/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 AA;
                                                                                                                                                                                                                                                                                              Vibrio cholerae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Guyongruaz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-1982;
                                                                                                                                                                                                                                                                                                                                                                                                      30-NOV-1983.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Milhaud G,
                                                                                                                                                                                                                                                                                                                                                  EP95426-A.
                                                    AAP30265;
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Gaps

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Query Match 100.0%; Score 39; DB 16; Length 23; Best Local Similarity 100.0%; Pred. No. 0.31; Matches 7; Conservative 0; Mismatches 0; Indels

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New synthetic polypeptide(s) for part of E. coli enterotoxin(s useful for vaccination of mammals against the enterotoxin(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 11; 13pp; French
                                                                                                                                               100.0%;
llarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                               83EP-0401052.
                                                                                                                                                                                                                                                                                                                                                                                                                                82FR-0009167.
                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-1983;
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                                                                                                                                                                                                                                                                                        21-APR-1992
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                                                                                                                        Sequence
                                                                                                                                                                                                                                                                      AAP30600;
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                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                       The repeating units are bonded together by intramolecular interpolypeptide cystine bonds formed between oxidized Cys residues of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. The composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys. X12 is Ala or Glu, X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP50439-57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Network polymer which comprises a series of composite E. coli heat-labile toxin (LT)/heat-stable toxin (ST) polypeptide repeating untis.
                                                                                                                                                                          New synthetic polypeptide(s) for part of E. coli enterotoxin(s useful for vaccination of mammals against the enterotoxin(s)
                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                            DB 6; Length 41; 0.55;
                                                                                                                                                                                                                                                                                                                                              0; Indels
         Heat-labile enterotoxin; heat-stable toxin; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heat-labile enterotoxin; heat-stable toxin; vaccine;
                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 39;
Best Local Similarity 100.0%; Pred. No. 0
Matches 7; Conservative 0; Mismatche
                                                                                                                                                                                                      Claim 8; Page 100; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                              AAP50436 standard; protein; 46 AA.
                                                                                  84WO-US02030.
                                                                                                    83US-0559469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84WO-US02030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83US-0559469
                                                                                                                      (SCRI-) SCRIPPS CLINIC RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SCRI-) SCRIPPS CLINIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                        WPI; 1985-159230/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1985-159230/26.
                                                                                                                                                                                                                                                                                                 41 AA;
                                                                                                                                                                                                                                                                                                                                                                           |||||||||
|15 evpgsqh 21
                                                                                                                                                                                                                                                                                                                                                               1 EVPGSQH 7
                                                                                 12-DEC-1984;
                                                                                                    12-DEC-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-DEC-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-DEC-1983;
                                             WO8502611-A
                                                                                                                                       Houghten RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-1985.
                                                                20-JUN-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO8502611-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houghten RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP50436;
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The inventors claim cholera toxin Bi subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coli (enterotoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as a vaccine 1-10mg of active cpd.
                                                                             The repeating units are bonded together by intramolecular interpolypeptide cystine bonds formed between oxidized cys residues of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins. The composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala or Glu, X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP50439-57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of amino acids 350-75 of the cholera toxin B1 subunit which carries an Arg at posns. 35, 67 and 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera vaccine; therapy; E.coli infection; enterotoxin LT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dodin A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rivaille P, Siffert O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 6;
Pred. No. 0.62;
Mismatches 0
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Claim 8; Page 100; 120pp; English.
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Involving analysis of the 3-dimensional form of the crystalline involving analysis of the 3-dimensional form of the crystalline holotoxin. The pertursis holotoxin modification process comprises:

(1) identification of at least one amino acid (aa) residue of the holotoxin for modification by analysing the 3-dimensional form of the crystalline holotoxin, in relation to known information of the protein structure and function; (2) effecting mutagenesis (by removing or replacing a nucleotide sequence encoding at least one (aa)) of a tox operon; and (3) expressing mutant tox box in a Bordetella organism to produce the modified holotoxin. This method is used for modifying pertussis holotoxin, by studying its 3-dimensional crystalline structure. Modifying the holotoxin, alters its blological properties. By analysing the 3-dimensional crystalline structures of the pertussis holotoxin can be identified. This can be used to predict (aa) which affect blological properties of the pertussis holotoxin can be identified. This can be used to predict (aa) which affect blological properties of the pertussis holotoxin. The present sequence represents an ADP-ribosylating toxin and a problem of the pertussis holotoxin. The present sequence represents an ADP-ribosylating toxin and a problem.
                                                                                                                                                                            ADP-ribosylating toxin; PT; crystalline pertussis holotoxin; ETA; DT; three-dimensional structure; LT; immunoprotective; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New method for producing modified pertussis holotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cockle SA, Loosmore S,
                                                                                                                                       Escherichia coli verotoxin-1 B-subunit.
                    AAY41816 standard; peptide; 93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Fig 5; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                 93US-0110947.
94US-0251121.
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                                                                                                08-DEC-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stein PE,
Oomen RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-579908/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 AA;
                                                                                                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
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31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-1994;
                                                                                                                                                                                                                                                                            US5965385-A
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Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Invention
                                                             AAY41816;
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    AAY41816
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                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR72540-R72545 are structurally equivalent B-subunits from three ADP-ribosylating toxins, pertussis holotoxtin (PT), E. coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify sites which contribute to PT's blological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New modified forms of pertussis holotoxin - developed using crystalline forms of pertussis holotoxin and its complexes with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Oomen R, Read RJ, Stein PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39; DB 16; Length 93; Pred. No. 1.3;
                                                       Query Match 100.0%; Score 39; DB 4; Length 47; Best Local Similarity 100.0%; Pred. No. 0.64; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                ADP-ribosylating toxin; pertussis holotoxin; B-subunit; active site; E. coli heat labile toxin; verotoxin-1; Bordetella pertussis vaccines.
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0
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                                                                                                                                                                                                                                                                          AAR72545 standard; peptide; 93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 5; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
100.0%;
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94US-0251121.
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                                                                                                                                                                                                                                                                                                                                                    28-NOV-1995 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-132623/18.
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Best Local Similarity
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47 AA;
                                                                                                                                                           1111111
23 evpgsqh 29
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                                                                                                                                     1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria sp
                                                                                                                                                                                                                                                                                                               AAR72545;
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  Sequence
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Armstrong GD;

Klein MH,

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                                Gaps
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0
 Length 93;
                                Indels
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0
Query Match 100.0%; Score 39; DB 20; Best Local Similarity 100.0%; Pred. No. 1.3; Matches 7; Conservative 0; Mismatches 0;
                                                                                                                                                                  AAW95226 standard; peptide; 93 AA.
                                                                                                                                     RESULT 15
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ID AAW9
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RESULT

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Pertussis toxin; heat labile toxin; verotoxin; exotoxin A; holotoxin; diphtheria toxin; ADP-ribosylating toxin; mannose binding protein; infection; crystal structure; X-ray crystallography; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crystalline form of isolated pertussis holotoxin useful in studying proteins which have functional resemblance
Heat labile toxin B subunit SEQ ID NO:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 5; 42pp; English.
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                                                                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                           immunogenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-1994;
                                                                                                                                                                                                                                                                                                            US6018022-A.
                                                                                                                                                                                                                                                                                                                                                                                25-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Read RJ,
Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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   NAME OF THE PROOF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modifications to e.g. enzymatic activity, mitogenicity and cell binding of pertussin holotoxin - by identifying interaction sites of a molecule with crystalline toxin and modifying the identified site
                                                                                                                                                                                                Pertussis holotoxin; PT; modified; effector; toxicity; cell binding; enzyme; ADP-ribosylation; toxin; crystalline; X-ray crystallography; structural analysis; interacting site; mitogenicity; adjuvanticity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 39; DB 20; Length 93; 100.0%; Pred. No. 1.3; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                E. coli heat-labile toxin (LT) beta-subunit sequence.
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Read RJ, Stein PE;
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93US-0110947.
94US-0251121.
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                                                                (first entry)
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Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYAL-) UNIV ALBERTA.
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                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
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                                                                                                                                                                                                                                                                                                            heat-labile; LT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Armstrong GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-1994;
                                                                16-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                         US5856122-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JAN-1999
AAW95226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY68365;
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AAY68365
ID AAY6
NAME OF THE PROOF OF THE PROOF
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Armstrong GD;

Klein MH,

Cockle SA, Loosmore S,

Stein PE, Oomen RP;

95US-0467976

93US-0110947 94US-0251121

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The present invention describes a crystalline form of isolated pertussis holotoxin, in which the molecules of pertussis toxin have pertussis holotoxin, in which the molecules of pertussis toxin have complexed with a polysaccharde molecule capable of forming a comparable with the holotoxin. The crystalline form of the pertussis holotoxin can be used in a comparison with other proteins which have functional resemblance to pertussis holotoxin with the aim of modifying other proteins. Identifying the unknown sites of toxicity by comparison with the three dimensional structure of pertussis holotoxin provides a technique for detoxification of toxins to produce useful immunogenic but non-toxic analogues. It can also be used as a primary standard to measure the quantity, purity or efficacy of less pure compositions containing pertussis toxin. AAY68340 to AAX68385 represent peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pertussis toxin; crystal structure; whooping cough; biological activity; lymphocytosis-promoting factor; histamine-sensitising factor; islet-activating protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 39; DB 21; Length 93; 100.0%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E coli verotoxin-1 B subunit SEQ ID NO: 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB66239 standard; Protein; 93 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVPGSOH 7
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The inventors claim vaccines against cholera and heat-labile E.coli toxin contg. cholera toxin fragment coupled to carrier. The toxin is esp. the fragments defined in FT, above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant constructs for expressing and opt. secreting proteins in Bordetella - comprise Bordetella promoter coupled to non-Bordetella, esp. cholera B toxin, gene or coupled to non-Bordetella leader and gene of interest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cholera toxin B subunit; enzyme; antigen; immunogen; allergen; enzyme inhibitor; hormone; lymphokine; immunoglobulin; toxin; structural protein; receptor; heterologous gene; leader; promoter.
                                                                                                                                                                            coli toxin - contg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant constructs comprising a promoter functional in Bordetella operatively linked to a heterologous gene or a non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bordetella pertussis; whooping cough; recombinant construct;
                                                                                                                                                                                                                                                                                                                                                                        6; Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GR;
                                                                                                                                                                                                                                                                                                                                                                        DB 6
1.4;
                                                                                                                                                                              Vaccines against cholera and heat-labile E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zealey
                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 39; DB
100.0%; Pred. No. 1.4
:ive 0; Mismatches
                                                                                                                                                                                               cholera toxin fragment coupled to carrier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Loosmore SM, Yacoob RK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Figure 1; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW04857 standard; Protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic cholera toxin B subunit.
                                                                                (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                             Example; Fig 1; 24pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96WO-CA00107
                84DE-3430894
                                                83IL-0069558
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Best Local Similarity 100.vv
These 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1996-425088/42.
                                                                                                                                              WPI; 1985-069683/12
                                                                                                                                                                                                                                                                                                                           103 AA;
                                                                                                                Arnon R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT38038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 evpgsqh 57
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVPGSQH 7
                  22-AUG-1984;
                                                  23-AUG-1983;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW04857;
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                                                                                                              Sela M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
AAW0485
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                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention provides a method for producing a pertussis toxin (also designated lymphocytosis-promoting factor, histamine-sensitising factor and islet activating protein) with a modified biological activity, involving analysing the crystal structure of the protein to identify active sites which can then be modified. This may lead to an alteration in the toxicity, cell binding or enzyme activity of the toxin. This can be used in the production of immunoprotective analogues of pertussis toxin is the cause of whooping cough following infection by Bordetella pertussis.
                                                                                                                                                                                                                                                                                                       Modifying pertussis holotoxin to produce detoxified PT analogs, comprising analyzing crystalline structure of toxin, to identify sites of toxicity, cell binding or enzyme activity of PT and modifying
                                                                                                                                                                                                                             Armstrong GD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                             Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 22;
Pred. No. 1.3;
Mismatches 0;
                                                                                                                                                                                                                             Loosmore S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine; cholera; heat-labile E.coli toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence of sub-unit B of cholera toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP50340 standard; protein; 103 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "claimed"
45..64
/note= "claimed"
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/note= "claimed"
                                                                                                                                                                                                                             Oomen RP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Fig 5; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 7; Conservative 0;
                                                                                            98US-0082514
                                                                                                                             94US-0292968
                                                                                                                                           93US-0110947
94US-0251121
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                                                                                                                                                                                           (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                           Cockle SA,
                                                                                                                                                                                                                                                                         WPI; 2001-122260/13
                                                                                                                                                                                                                                            Stein PE;
Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93 AA;
                                                                                                                                                                                                                                                                                                                                                         identified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vibrio cholera
                               US6168928-B1
                                                                                             21-MAY-1998;
                                                                                                                             22-AUG-1994;
                                                                                                                                           24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DE3430894-A.
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                                                              02-JAN-2001
                                                                                                                                                                                                                          Read RJ,
Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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AAP50340 RESULT

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Gaps

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CI-B

plant. The immunogenic agent preferably comprises the LT-B or (cholera toxin B subunit) or optionally LT-A or CT-A.

103 AA;

Sequence

SSXS

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Bordetella leader sequence for secretion of a gene product which may cor may not be of Bordetella origin, can be used for the expression in Dordetella of Enzymes, antigens, immunogens, allergens, enzyme inhibitors, hormones, immunoglobulins or their fragments, toxins, mammalian proteins, structural proteins or their receptors. The Bordetella strains are particularly engineered to express the cholera toxin B subunit (this sequence). The promoters used in the constructs are selected from the Bordetella pertussis tox, that promoters or the high molecular weight (hmw) outer membrane promoter of non typable Haemophilus influenzae; leaders used in the constructs are selected from the cholera toxin B leader (CTB-L), the pertussis toxin subunit 31 leader (S1-L) and the pertussin pertactin leader (PRN-L); and genes used in the constructs are selected from a constructs are selected from a convel synthetic cholera toxin B gene (ctb) and the hmwl and hmw2
                                                                                                                                                                                                                                                                                                                                                                                                                         genes of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 AA;
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Query Match 100.

Best Local Similarity 100.

Matches 7; Conservative 1 EVPGSQH 7 ò ద

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Gaps

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0; Indels

Mismatches

; 0 100.0%;

Score 39; DB 17; Length 103; Pred. No. 1.4;

AAR94939 standard; Protein; 103 AA.

AAR94939;

31-0CT-1996

Toxin; subunit; vaccine; transgenic plant; immunogen; antigen; adjuvant; immunisation. Heat labile enterotoxin B subunit (LT-B) E.coli (first entry) Escherichia coli. 

95WO-US13376. 94US-0328716 WO9612801-A1 24-OCT-1995; 24-OCT-1994; 02-MAY-1996

(TULA ) TULANE EDUCATIONAL FUND. (TEXA ) UNIV TEXAS A & M SYSTEM.

Clements JD, Hag TA, Arntzen CJ,

Mason HS;

N-PSDB; AAT18799, AAT18800 WPI; 1996-230602/23

Transgenic

nsed

Disclosure; Page 100-101; 130pp; English.

sgenic plants contg. E. coli heat labile enterotoxin subunits as oral vaccines for animals which consume the plant

an immunogenic agent can be be used as an oral vaccine for animals. The vaccine is administered by the oral consumption of the plant and provides the first known functional method for immunising animals using transgenic plants, where the plants express bacterial antigens that act as both immunogens and adjuvants. The method provides an inexpensive production and delivery system for such antigens to animals. This is the LT-B Escherichia coli toxin subunit and its coding sequence was used in the construction of such a transgenic A transgenic plant comprising or expressing a DNA sequence encoding

Gaps Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; CTB; heat labile enterotoxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea; AAW06606 is a mature cholera toxin B subunit (CTB)/heat labile enterctoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid. Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness ö Length 103; Indels /label= substitution /note= "wild-type His replaced by Asn" Misc-difference 95 /label= substitution /note= "wild-type Thr replaced by Ala" /label= substitution /note= "wild-type Ala replaced by Ser" ö 100.0%; Score 39; DB 17; 100.0%; Pred. No. 1.4; Chimeric - Vibrio cholerae. Chimeric - Enterotoxigenic Escherichia Coli. 0; Mismatches Location/Qualifiers AAW06606 standard; Protein; 103 AA. Claim 3; Page -; 32pp; English. 96WO-SE00570. 95SE-0001682 Query Match Best Local Similarity 100.00 Best Local 7; Conservative 06-AUG-1997 (first entry) vomiting; food poisoning. Holmgren J, Lebens MR; WPI; 1996-506108/50. Misc-difference 94 Misc-difference 1 (HOLM/) HOLMGREN (LEBE/) LEBENS M N-PSDB; AAT43576 51 evpgsqh 57 1 EVPGSQH 7 02-MAY-1996; 05-MAY-1995; WO9634893-A1 37-NOV-1996 AAW06606; RESULT 2 ò qq 

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AAW06605)
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(MCGH/) N
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                                                                                                                                                                                                                                                                                                                     RESULT
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                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW06607 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB protein, certain amino acids (aa) were replaced with corresponding aa from heat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to
protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vocine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.

Note - This sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                                                                                                                                                                                                     Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 1..25
/label= substitution
/label= "the first 25 amino acids of mature
/note= "the first 25 amino acids of mature
wild-type cholera toxin B subunit are
replaced with the first 25 amino acids
of mature enterotoxin B subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                       ·,
                                                                                                                                                          Score 39; DB 17; Length 103; Pred. No. 1.4;
                                                                                                                                                                                       Indels
                                                                                                                                                                                       ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric - Vibrio cholerae.
Chimeric - Enterotoxigenic Escherichia Coli.
                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                 AAW06607 standard; Protein; 103 AA.
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                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95SE-0001682
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vomiting; food poisoning
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1996-506108/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT43577
                                                                                                                                                                                                                                             51 evpgsqh 57
                                                                                                                   103
                                                                                                                                                                                                                 1 EVPGSQH 7
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                                                                                                                                                                                                                                                                                                                                                                           06-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-NOV-1996
                                                                                        AAW06605)
                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                             AAW06607
                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                    AAW06607
                                                                                                                                                                                                                                                                                        RESULT
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This is the amino acid sequence of the cholera toxin B subunit used in the method of the invention involving the use of nontoxic subunits as an effective adjuvant in coadministration of an antigen to birds and animals. In addition to the use of the toxin as an mucosal adjuvant, it also provides a vaccine comprising the toxin, an immunogenic amount of an antigen, and a pharmaceutically acceptable carrier. The toxin can be used with single/multiple vaccines, and it enables the possibility for commercial mucosal adjuvants for use in humans, since these are more effective and safer than vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera toxin B subunit; nontoxic subunit; adjuvant; coadministration;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mutant cholera toxin selected from a group comprising nontoxic subunits/derivatives - effective as an adjuvant when coadministered
immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness, e.g. diarrhoea and vomiting, in humans and animals.

Note - This sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of the wild type chorela toxin B subunit.
                                                                                                                                                                                                                                                                                                                                                                                        Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB 17;
Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen; bird; animal; mucosal; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with an antigen to birds and mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW80808 standard; protein; 103 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; F1g 1B; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takeda Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                administered subcutaneously:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KIYONO H.
MCGHEE J R.
TAKEDA Y.
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
'The 7; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YAMAMOTO S
                                                                                                                                                                                                                                                                                                      A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vibrio cholerae.
                                                                                                                                                                                                                                                                                                   103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 evpgsqh 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-APR-1998;
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103 AA;

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B subunit of the heat-labile enterotoxin (LT-B) derived from E. coli.
                                                   B subunit; heat-labile enterotoxin; LT-B; Escherichia coli; malari; circumsporozoite protein; fusion protein; live recombinant vaccine; Salmonella; epitope.
                                                                                                                                                                                                                                                                                                             Live recombinant vaccine for malaria - comprising attenuated entero-invasive bacterium contg. DNA
                                                                                                                           ....signal peptide"
23..124
/note="Mature LT-B"
                                                                                                                                                                                                                                                                                                                               encoding epitope of malaria parasite
                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                             Majarian WR, Pillai S,
                                                                                                                                                                                                                                                                                                                                                 Fig 3; p. 3/17; 105pp; English
                                                                                                                                                                                                       88WO-US03376.
                                                                                                                                                                                                                           87US-0104735.
                                                                                                                                                                                                                                            (PRAX-) PRAXIS BIOLOGICS IN.
                 06-JUN-1990 (first entry)
                                                                                                                                                                                                                                                                                WPI; 1989-114399/15.
N-PSDB; AAN90747.
                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        evpgsqh 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVPGSQH 7
                                                                                                                                                                                                       30-SEP-1988;
                                                                                                                                                                                                                           02-OCT-1987;
                                                                                                                                                                   WO8902924-A
                                                                                                                                                                                      06-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                             multivalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
AAP93561;
                                                                                                                                                                                                                                                               Brey RN,
                                                                                                                     Peptide
                                                                                                                                       Protein
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Ob
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                                                                                                                                                                                               cholera toxin B-subunit; hybrid protein; heterologous IgA active antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mature cholera toxin B-subunit is obtained when the signal peptide is cleaved off. There is an Ochre codon at position 343-5; the sequence downstream from it is part of a plasmid.
                                    Gaps
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          New hybrid protein, useful in vaccines -contains cholera toxin b subunit and heterologous IgA active antigenic sequence.
                100.0%; Score 39; DB 19; Length 103; 100.0%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 39; DB 11; Length 118; 100.0%; Pred. No. 1.6;
                                    Indels
                                                                                                                                                                                                                                                                1..11
/*label- signal peptide
/*note- absent from mature protein
                                   ;
0
                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            (UYLI-) L'UNIVERSITE DE L'ETAT A LIEGE.
                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                      AAR04163 standard; protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                              Martial
                                                                                                                                                                                                                                                                                                                                       89WO-0000495.
                                                                                                                                                          (first entry)
                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; ; pp; French.
                                                                                                                                                                             Cholera Toxin B-subunit.
                                                                                                                                                                                                                                                                                                                                                                                              Renard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
'-heq 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1990-132273/17.
N-NSDB; Q04046.
                         Best_Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 AA;
                                                                                                                                                                                                                                            misc_difference
                                                                1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                       27-SEP-1989;
                                                                                                                                                          10-SEP-1990
                                                                                                                                                                                                                                                                                                   WO9003437-A.
                                                                                                                                                                                                                                                                                                                     05-APR-1990.
                                                                                                                                                                                                                                                                                                                                                                                              L'Hoir C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                 synthetic
                                                                                                                                       AAR04163;
                  Query Match
                                                                                                                                                                                                                                                               region
                                                                                                  RESULT 24
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Hockmeyer WT;

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In the patent, the DNA encoding LT-B is expressed as part of a fusion protein with an epitope of a malaria parasite, eg Region I or Region II or a repeat region of circumsporozoite protein antigen (CS) (AAP93560) from Plasmodium berghei. Pref. the fusion gene is inserted into attenuated Salmonelia enteriditis under the left promoter control of ambda. Such bacteria can multiply in the host without causing disease or disorder and express CS that will induce a protective immune response against malaria and can be used in vaccines. Such vaccines can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 39; DB 10;
ilarity 100.0%; Pred. No. 1.7;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: July 16, 2001, 16:35:41 Job time: 205 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
Matches 7; Conserv
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Gaps

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0; Mismatches

Conservative

evpgsqh 68

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1 EVPGSOH 7

AAP93561 standard; protein; 124 AA.

RESULT 25 AAP93561

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Appli Appli Appli Appli Appli Appli

Sequence 1, A Sequence 2, A Sequence 2, A Sequence 2, A Sequence 6, A Sequence 6, A Sequence 6, A Sequence 4, A Se

Appl Appli Appli Appli Appli Appli Appli Appli

Seguence Sequence Sequence 2, Sequence 7,

us-09-786-648-2.rai

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TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,968
US-08-714-070A-1
US-08-045-806-2
US-08-045-806-2
US-08-56-05-6
US-08-56-05-6
US-08-56-05-6
US-08-56-05-6
US-08-56-05-6
PCT-US95-11684-4
US-08-602-359A-34
US-08-602-359A-34
US-08-602-359A-34
US-08-602-359A-34
US-08-903-379-4
US-08-906-752B-4
US-08-906-752B-2
US-08-906-752B-2
US-08-906-752B-2
US-08-906-752B-2
US-08-906-752B-2
US-08-96-752B-2
US-08-96-752B-2
US-08-96-752B-2
US-08-96-752B-2
US-08-96-752B-2
US-08-96-752B-2
US-08-96-752B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAX-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 26, Application US/08292968
| Patent No. 5856122
| GENERAL INFORMATION:
| APPLICANT: READ, Randy J. APPLICANT: COCKLE, Stephen A. APPLICANT: OOMEN, RAYMOND P. APPLICANT: LOOSMORE, Sheena | APPLICANT: REIN, Michel H. APPLICANT: ARMSTRONG, Glen D. APPLICANT: HAZES, Bart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Suite 701, 330 Univers
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 100
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEC ID NO. 26;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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805
805
1285
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       Patent No. 5223610
Sequence 9, Appli
Patent No. 5194375
Patent No. 5194375
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Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
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Sequence 8, Appli
Sequence 8, Appli
Patent No. 5194375
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Sequence 2, Appli
Sequence 21, Appl
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Sequence 4, Appli
Sequence 12, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Appli
                                                                                                                    July 16, 2001, 16:32:51 ; Search time 30.3 Seconds (without alignments) 4.654 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 21, A
Sequence 1, Al
Sequence 2, Al
Sequence 2, Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26,
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/cgg2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgg2_6/ptodata/2/jaa/6A_COMB.pep:*
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/cgg2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
/cgg2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-467-536-26
US-08-67-536-26
US-08-952-337-5
US-08-952-337-6
US-08-952-337-6
US-08-952-337-6
US-08-952-337-6
US-09-013-047-2
US-09-013-047-2
US-09-013-047-2
US-09-191-852-21
US-09-191-852-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-435-605A-12
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US-08-694-078-8
US-09-058-260-8
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US-08-449-045C-4
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US-08-952-337-2
US-08-747-410-2
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                                                                                                                                                                                                                                                                                                                                    193259 seqs, 20144635 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maximum Match 100%
Listing first 45 summaries
                                                                                             OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
                                                                                                                                                                                              US-09-786-648-2
39
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Match Length DB
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2262
3262
329
329
539
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                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                    Searched:
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                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: STEIN, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COOSNORE, Sheena
APPLICANT: LOOSNORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING APPLICATION 435

PRIOR APPLICATION TA:

APPLICATION TA:

FILING APPLICATION AND TA:

APPLICATION NUMBER:

RICK APPLICATION DATA:

APPLICATION NUMBER:

FILING APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

FILING APPLICATION NUMBER:

AND AND APPLICATION NUMBER:

ATTORNEY APPLICATION NUMBER:

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-455 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                    ; Sequence 26, Application US/08467536
; Patent No. 5977304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEO ID NO: 26
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Toronto
STATE: Ontario
                                                                          1111111
41 EVPGSQH 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1111111
41 EVPGSQH 47
                                   1 EVPGSQH 7
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US-08-467-536-26
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US-08-467-976-26
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                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                               100.0%; Score 39; DB 2; Length 93; 100.0%; Pred. No. 0.56; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 39; DB 2; Length 93; Best Local Similarity 100.0%; Pred. No. 0.56; Matches 7; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: READ, Randy J.
APPLICANT: READ, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: OOMEN, Raymond P.
APPLICANT: COCSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBURNEY
STREET: Suite 701, 330 University Avenue
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/467,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-454 MIS:VG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/291,121
FILING DATE: 22-NGG-1994
PRIOR APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-NAX-1994
PRIOR APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-NGG-1993
FILING DATE: 24-NGG-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/08467974
Patent No. 5965385
                                                                                               Query Match
Best Local Similarity 100.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: READ, 1
                                                                                                                                                                                                                                                                               1111111
41 EVPGSQH 47
                                                                                                                                                                                                                                     1 EVPGSQH 7
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US-08-467-974-26
US-08-292-968-26
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Sequence 5, Application US/08952337

Sequence 5, Application US/08952337

Sequence 5, Application US/08952337

Setent No. 6019973

GENERAL INFORMATION:
APPLICANT: Holmaren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
CURRENT APPLICATION NUMBER: US/08/952,337

CURRENT APPLICATION NUMBER: PCT/SE96/00570

EARLIER FILING DATE: 1996-05-02

EARLIER APPLICATION NUMBER: SE 9501682-0

EARLIER PILING DATE: 1995-05-05

NUMBER OF SED ID NOS: 6

SOFTWARE: FASLSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 39; DB 4; Length 93; 100.0%; Pred. No. 0.56; 1.ive 0; Mismatches 0; Indels
                             APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
WUMBER OF SOUGHNES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                  STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENTING NUMBER: US/09/082,514
FILING DATE:
                                                                                                                               E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
1 24 - ANG-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-810
TELECOMMONICATION INFORMATION:
TELEPHONE: (416) 595-1155
       APPLICANT: ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26;
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: Vibrio cholerae US-08-952-337-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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41 EVPGSQH 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVPGSOH 7
                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 5
LENGTH: 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
US-08-952-337-5
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                                                                  APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKIE, Stephen A.
APPLICANT: COMEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: HALEN, Michel H.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MOBUTNEY
                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,976
FILING DATE: 05-JUN 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 06-UNN-1995
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-YAY-1994
PRIOR APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-YAY-1994
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
Sequence 26, Application US/08467976 Patent No. 6018022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-082-514-26
; Sequence 26, Application US/09082514
; Patent No. 6168928
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               READ, Randy J.
STEIN, Penelope E.
COCKLE, Stephen A.
OOMEN, Raymond P.
KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26.
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 EVPGSQH 47
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-467-976-26
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Gaps

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GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena M
APPLICANT: Yacoob, Reza K
APPLICANT: Zacob, Reza K
APPLICANT: Zaciby, Gavin R
APPLICANT: Zaciby, Gavin R
APPLICANT: Klein, Michel H
TITLE OF INVENTION: EXPRESSION OF GENE PRODUCTS FROM
TITLE OF INVENTION: GENETICALLY MANIPULATED STRAINS OF BORDETELLA
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 2; Length 103; Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,526
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 2;
Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08894526 Patent No. 5942418
                                            NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
100.0%;
                                                                                                                                                                                                   ..... 103 amino acids
TYPE: amino acids
TOPOLOGY: 157-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                  TELEFAX: 416-595-1163
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : 103 amino acids
amino acid
                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: protein US-08-472-171-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6th Floor
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                   Gaps
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APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Zealey, Gavin R.
APPLICANT: Kein, Michel H.
TITLE OF INVENTION: Expression Of Gene Products From VIMBER OF SEQUENCES: 56
CORRESPONDENCE: 56
CORRESPONDENCE ADDRESS:
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APPLICANT: HOLMATION:
APPLICANT: HOLMATION:
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILER REFERENCE: 346/00758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1996-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER PILING DATE: 1996-05-02
EARLIER PILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FRASELER PLICATION NUMBER: SE
SOFTWARE: FASTESQ FOR WINDOWS VERSION 3.0
LENGTH: 102
Score 39; DB 3; Length 102;
Pred. No. 0.62;
Mismatches 0; Indels
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STREET: 330 University Avenue, Suite 701
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/472,171
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Patent No. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08472171 Patent No. 5932714 GENERAL INFORMATION:
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  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT; ORGANISM: Escherichia coli
US-08-952-337-6
Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                              1111111
50 EVPGSQH 56
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50 EVPGSQH 56
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US-08-952-337-6
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Gaps
                     APPLICANT: Zealey, Gavin R.
PAPLICANT: Klein, Michel H.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Charles J. Arntzen, Hugh S. Mason, and Tarig A. Hag
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski L.L.P.
STREET: 1301 MCKinney, Suite 5100
CITY: HOUSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                           STATE: OUTUATION
STATE: ONTAINO
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,597
FILING DATE: CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNBER: 08/393,334
FILING DATE: FEBRUARY 23, 1995
CLASSIFICATION:
AMPLICATION OF THE TRANSMARY 23, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.62;
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ZIP: 77010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                             E: Sim & McBurney
330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1038-964
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Patent No. 6194560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFRENCE/CDCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1153
TELERAX: 416-595-1163
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
  Yacoob, Reza K.
Zealey, Gavin R.
Klein, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 103 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: Ilnear
; MOLECULE TYPE: protein
US-09-374-597-2
                                                                                                                NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCB
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51 EVPGSQH 57
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US-09-191-852-21
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    Gaps
                                                                                                                                                                                                                                                                  APPLICANT: LOSSMOTE, Sheena M.
APPLICANT: LOSSMOTE, Reza K.
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-507 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
TELEFAX: 416-595-1163
TELEFAX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/472,171
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/393,334
FILING DATE: 23-FEB-1995
ATTORNEY-AGENT INFORMATION:
NAME: Stewart, Michael I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/013,047 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                      Sequence 2, Application US/09013047 Patent No. 5998168 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09374597
Patent No. 6140082
GENERAL INFORMATION:
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7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-09-013-047-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 330 UniveCITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
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                                                                                      51 EVPGSQH 57
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51 EVPGSQH 57
                                             1 EVPGSQH 7
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Matches
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Gaps

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APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN B SUBUNITS
FILE REFERENCE: 3846/0D78
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1996-05-02
EARLIER FILING DATE: 1996-05-02
EARLIER FILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FatSEQ for Windows Version 3.0
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Sequence 2, Application US/08952337
Sequence 1. Mornarion
Sequence 1. Mornarion
Sequence 2. Mornarion
Sequence 2. Mornarion
Sequence 3. Morn
                                                                Query Match 100.0%; Score 39; DB 5; Length 103; Best Local Similarity 100.0%; Pred. No. 0.62; Matches 7; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08952337 Patent No. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Eschcerichia coli
US-08-952-337-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT; ORGANISM: Vibrio cholerae US-08-952-337-1
                                                                                                                                                                                                                                                                                           51 EVPGSQH 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 EVPGSQH 77
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LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                              15-08-952-337-1
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APPLICANT: 310 Wisenbaker
APPLICANT: College Station, Texas 77843-3369
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 39; DB 4; Length 103; 100.0%; Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                              FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
FILING DATE: 24-OCT-1995
APPLICATION NUMBER: 08/817,906
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER:
TLING DATE: 24-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jones, John W.
REGISTRATION NUMBER: 36170/3P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 713-850-0909
                                                                                                                                                                                                                                                                                                                     NAME: FOX, DAVIG L.
REGISTRATION NUMBER: 40,612
REFERENCE/POCKET NUMBER: P01590US1
TRIECOMUNICATION INFORMATION:
TELEPHONE: 713-651-5151
APPLICATION NUMBER: US/09/191,852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
PCT-US95-13376-21
Sequence 21, Application PC/TUS9513376
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 713-651-5246
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 103 amino acids
amino acid
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Best Local Similarity 100.
Matches 7; Conservative
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51 EVPGSQH 57
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Patent No. 5770203
GENERAL INFORMATION:
APPLICANT: Burnette, Neal W.
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF SEQUENCES:
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
STARET: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 39; DB 2; Length 371; 100.0%; Pred. No. 2.4;
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COUNTRY: USA

ZIP: 91320-1789

ZIP: 91320-1789

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,045C

PTITING DATE: 24-MAY-1995
                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/829,026A FILING DATE: 18-AUG-1997 CLASSIFICATION: 435
                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
STREET: Room 411, Building 005, BARC-W
CITY: Beltsville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATE: 24-MAI ACCEPTING DATE: 24-MAI ACCEPTING DATE: 24-MAI ACCEPTION: 424
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/694,733
APPLICATION NUMBER: US 07/694,733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 02-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-504-5676
FORMATION: 301-504-5060
                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIÚM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Gracter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 371 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 301-504-5060
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-08-829-026A-6
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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55 EVPGSQH 61
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US-08-449-045C-4
                                                                                                                                                                            COUNTRY:
                                                                                                                  CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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; Sequence 6, Application US/08829026A
; Patent No. 2837825
; Patent No. 2837825
; GENERAL INFORMATION:
   APPLICANT: Meinersmann, Richard J.
   APPLICANT: Khoury, Christian A.
   TITLE OF INVENTION: Campylobacter Jejuni Flagellin-Escherichia Coli LT-B Fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 0.76;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,410
FILING DATE: 12-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATE:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 11526
TELECOMMUNICATION INFORMATION:
""" INFERPENCE TO THE TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   internal
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TELEX:
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-747-410-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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72 EVPGSQH 78
                                                         1111111
71 EVPGSQH 77
                           1 EVPGSQH 7
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APPLICANT: Karathanasis, Sotirios K.
APPLICANT: Ladias, John A.
APPLICANT: Rottman, Jeffrey N.
APPLICANT: Widom, Russell L.
TITLE OF INVENTION: Control of the Apolipoprotein AI Gene
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STARET: Massachusetts
COUNTRY: 02173.
  5223610-3
;Patent No. 5223610
; APPLICANT: Burton, Frank H.;Sutcliffe, Gregor
; TITLE OF INVENTION: CHOLERA TOXIN GENE REGULATED BY GROWTH
                                                                                                                                                                                                                                                                                                      Score 33; DB 6; Length 124;
Pred. No. 11;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.5%; Score 31; DB 1; Length 414; 100.0%; Pred. No. 1e+02; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/255,471
FILIG DATE: 08-JUN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/784,472
FILING DATE: 24-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Alice 0.
REGISTATION NUMBER: 33,542
REFERENCE/DOCKET NUMBER: CMCC-234A
TELECOMMUNICATION INFORMATION:
                                                                                        HORMONE PROMOTER
NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/528,852
FILING DATE: 18-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 21
US-08-255-471-9
. Sequence 9, Application US/08255471
; Patent No. 5721096
                                                                                                                                                                                                                                                                                                             84.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 414 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        72 EVPSSQH 78
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                                                                                                                                                                                                                         LENGTH: 124
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                                                                                                                                                                                                     SEQ ID NO:3
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GENERAL INFORMATION:
APPLICANT: Burnette, W. Neal
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ...
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Pred. No. 11;
0; Mismatches 1; Indels
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Pred. No. 11;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/435,605A

FILING DATE: 05-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . А-196В
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US-08-435-605A-12
Sequence 12, Application US/08435605A
; Patent No. 5874287
ATTORNEY AGENT INFORMATION:
NAME: MAZZA, RICHARG 17, 657
REGISTRATION NUMBER: 27, 657
REFERNEK POCKET NUMBER: A-19;
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
LENGTH: 124 amino acids
TOPOLOGY: 1inear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 05-MAY-1995
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: MAZZA, RICHARD J.
REGISTRATION NUMBER: 27,657
REFERENCE/POCKET UNMBER: A-196
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                           84.6%;
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TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-449-045C-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-435-605A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: California
COUNTRY: USA
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Sequence 8, Application US/08694078
Fatent No. 6218163
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALLEN, Larry
APPLICANT: ALKEN, John
APPLICANT: FONSTEIN, Machael
APPLICANT: DEMIRJIAN, David
APPLICANT: DEMIRJIAN, David
APPLICANT: ASADABAN, Malcolm
ITILE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
NUMBER OF SEQUENCES: 8
APPLICANT: CASADABAN, Malcolm
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 329;
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                                                                                                                                       COUNTRY:

21P: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Daystem: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,802
FTLING DATE: 10-JAN-1997
FTLING DATE: 10-JAN-1997
                                                                 ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 S. Wacker Drive 32nd Floor
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; L6
1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,580
FILING DATE: 12-UUN-1996
PROF APPLICATION DATA:
APPLICATION NUMBER: US 60/009,704
FILING DATE: 11-AN-1996
PRIOR APPLICATION UMBER: US 60/001,995
FILING DATE: 01-AUG-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37,293
¤¤R: 95,963-E
                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,078
FILING DATE: 07-AUG-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.9%; Sur
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Chao, Mark
REGISTRATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 95
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 329 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity luv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-781-802-8
                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                 COUNTRY: US' ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 PGSQH 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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US-08-694-078-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                           5194375-6; Patent No. 5194375; Patent No. 5194375; TITLE OF INVENTION: DNA ENCODING INTERLEUKIN-7 RECEPTORS AND TITLE OF INVENTION: DNA ENCODING INTERLEUKIN-7 RECEPTORS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: PARK, LINDA S.;GOODWIN, RAYMOND G.
TITLE OF INVENTION: DNA ENCODING INTERLEUKIN-7 RECEPTORS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 30; DB 6; Length 262;
Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 31; DB 6; Length 459;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                     CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/493,588

FILING DATE: 21-MAY-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 421,201

FILING DATE: 13-007-1989

APPLICATION NUMBER: 366,910

FILING DATE: 15-JUN-1989

SEQ ID NO:6:

LENGTH: 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/493,588
FILING DATE: 21-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,201
FILING DATE: 13-0CT-1989
APPLICATION NUMBER: 366,910
FILING DATE: 15-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-781-802-8
Sequence 8, Application US/08781802
Patent No. 5969121
GENERAL INFORMATION:
APPLICANT: ALLEN, Larry
APPLICANT: AIKENS, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AIKENS, John
FONSTEIN, Michael
VONSTEIN, Veronika
DEMIRJIAN, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.9%;
85.7%;
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85.7%;
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Best Local Similarity 85.7*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; METHODS OF USE
; NUMBER OF SEQUENCES: 9
                                                                                                                                                                                     METHODS OF USE

NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 EVDGSQH 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 1111
47 EVNGSQH 53
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                                 14 EVPGSQ 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Patent No. 5194375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO:4
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5194375-4
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Gaps

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Query Match 76.9%; Score 30; DB 4; Length 329; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 0; Indels
                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUARE: US/08/694,078
FILING DATE: 07-AuG-1996
CLASSIFICATION 373
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/019,580
FILING DATE: 12-JUN-1996
PRIOR APPLICATION NUMBER: US 60/009,704
FILING DATE: 10-JAN-1996
PRIOR APPLICATION NUMBER: US 60/001,995
FILING DATE: 10-JAN-1996
PRIOR APPLICATION NUMBER: US 60/001,995
ATORNEY/AGENT INFORMATION:
APPLICATION NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 37,293
REFERENCE/DOCKET NUMBER: 95,963-C
TELEFAX: 312-913-0001
FILEFAX: 312-913-0002
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHERARCFERISTICS:
LENGTH: 329 amino acids
TTPE: amino acid
TOPE: Inner Protein
US-08-694-078-8
CITY: Chicago
STATE: Illinois
COUNTRY: USA
2IP: 60606
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Search completed: July 16, 2001, 16:36:18 Job time: 207 sec

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Gaps

; 0

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                        OM protein - protein search, using sw model
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July 16, 2001, 16:33:31; Search time 34.9 Seconds (without alignments) 15.279 Million cell updates/sec Run on:

US-09-786-648-2 39 1 EVPGSQH 7 score: Title: Perfect so Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 Total number of hits satisfying chosen parameters:

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Maximum Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:* Database

pir1:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	rae	heat-labile entero	hypothetical prote	Ln 2	qlucarate dehydrat	žK112.1 protein -			protein F20B17.2 [	homeobox protein (	hypothetical prote		conserved hypothet	apolipoprotein A-I	apolipoprotein A-I	chorismate synthas			hypothetical prote			~	hypothetical prote	_	conserved hypothet	interleukin-7 rece	conserved hypothet	interleukin-7 rece	hypothetical prote
SUMMARIES	ID	XVVCB	QLECB	T14755	T01751	A69753	S44886	B27586	T34767	C96827	B48820	G84353	175446	381715	437133	148975	146725	T51020	34791	T26069	196719	129041	A43425	372782	T31701	D83638	134791	D83072	B34791	:84169
	DB	1						7										2							-		7			7
	Match Length D	124	124	272	367	455	534	137	242	260	273	274	353	374	414	414	432	432	459	489	1028	1258	. 1259	148	153	182	262	270	298	304
*	Match	100.0	100.0	84.6	84.6	82.1	82.1	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	79.5	76.9	6.94	76.9	76.9	76.9	76.9	76.9
	Score	39	39	33	33	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	30	30	30	30	30	30	30
+[::sog	NO.	1	7	m	4	ស	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	

DNA-directed RNA p probable 4-carboxy	probable 3-oxoadip chorismate synthas	hypothetical prote flavocytochrome C	hypothetical prote	4-aminobutyrate tr	anti-mullerian hor	hypothetical prote	scarecrow-like pro	hypothetical prote	thiamin repressibl	aryl hydrocarbon r
A72247 T47115	T35015 S17246	T47142 B70321	T44138	A34/91 JC4022	JC4335	T22716	T47874	T05041	S41962	A46266
77	7 7	77	~ ~	7 7	01 0	4 (4	7	7	7	7
336	375 376	412	440	500	573	622	623	619	775	802
76.9	76.9	76.9	76.9	76.9	76.9	76.9	6.94	76.9	76.9	6.97
30	30	30	30	30	30	30	30	30	30	30
30	32 33	3 3 4 3 5	36	38 38	98	41	42	43	44	45

## ALIGNMENTS

RESULT	-1			ď				
XVVCB				-				
cholera	cholera enterotoxin, B chain precursor VC1456 [valida	xin,	œ	chain	precurs	or	VC1456	[valida
N; Alter	N;Alternate names: enterotoxin beta chain	S: @	te	rotoxi	n beta	cha	in	

N;Alt

ted] - Vibrio cholerae (strain N

C; Species: Vibrio cholerae C; Date: 24-Apr-1984 #sequence_revision 01-Sep-2000 #text_change 02-Feb-2001 C; Accession: S14624; S39238; S39241; H82196; JC1078; S17666; PC1010; A05130; A01819; R; Dams, E.; de Wolf, M.; Dierick, W. Submitted to the EMBL Data Library, March 1991 A; Description: Correction of the cholera toxin nucleotide sequence of the Vibrio chol. A; Reference number: S14623

A;Accession: S14624
A;Molecule type: DNA
A;Residues: 1-124 cDAM>
A;Coss.references: EMBL:X58786; NID:g48420; PIDN:CAA41593.1; PID:g48422
A;Experimental source: strain 2125
A;Experimental source: strain 2125
B;Lebens, M.; Holmgren, J.
submitted to the EMBL Data Library, November 1993
A;Bescription: Structure and arrangement of the Cholera toxin genes in vibrio Cholera
A;Reference number: S39238

A; Accession: S39238

A; Molecule type: DNA A; Residues: 1-124 <LEB>

A;Cross-references: EMBL:X76390; NID:g433856; PIDN:CAA53973.1; PID:g433857

A; Accession: S39241

A; Molecule type: DNA A; Residues: 1-124 <LEW>

A;Cross-references: EMBL:X76391; NID:g433859; PIDN:CAA53976.1; PID:g433861
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-124 <HEI>

A; Cross-references: GB: AE004224; GB: AE003852; NID: 99655952; PIDN: AAF94613.1; GSPDB:GM A; Experimental source: serogroup O1; strain N16961; biotype El Tor R; Sh1, C.H.; Cao, C.; Zhang, J.S.; Ma, Q.J. Chinese Biochem. J. 9, 395-399, 1993 A; Title: Nucleotide sequence analysis of the gene encoding the classical biotype V.c. A; Reference number: JC1078

A; Accession: JC1078

A; Molecule type: DNA
A; Residues: 1-20, '0', 22-31, 'Q', 33-38, 'H', 40-49, 'G', 51-67, 'T', 69-124 <SHI>
A; Residues: 1-20, 'O', 22-31, 'Q', 33-38, 'H', 40-49, 'G', 51-67, 'T', 69-124 <SHI>
A; Experimental Source: classical biotype strain 569B
B; Dams, E.; de Wolf, M.; Dierick, W.
Biochim. Biophys. Acta 1090, 139-141, 1991
A; Title: Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classic
A; Reference number: S17665; MUID:91355224

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R;Dallas, W.S.; Falkow, S.
Nature 288, 499-501, 1980
A;Title: Amino acid sequence homology between cholera toxin and Escherichia coll hea—
A;Reference number: A01820; MUID:81074965
                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Reaidues: 11-14 cOhr.
A;Reaidues: 11-14 cOhr.
J. Bacteriol. 169, 1352-1357, 1987
A;Title: Evolutionary origin of pathogenic determinants in enterotoxigenic Escherich—
A;Title: Evolutionary origin of pathogenic determinants in enterotoxigenic Escherich—
A;Reference number: A26946; MUID:87137303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1.-27, E., 29-63, 'K', 65-124 <YAM>
A; Residues: 1.-27, E., 29-63, 'K', 65-124 <YAM>
A; Cross references: EMBL: M15365; NID:9148335; PIDN:AAA24792.1; PID:9148336
B; Leong, J.; Vinal, A.C.; Dallas, W.S.
Infect. Immun. 48, 73-77, 1985
A; Title: Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons=
A; Reference number: 141194; MUID:85156481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-5, F', 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17, 7-17
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A; Residues: 1-17, 'C', 19, 'Y', 21-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-122, 'E', 124
A; Residues: 1-17, 'C', 19, 'Y', 21-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-122, 'E', 124
A; Cross-references: GB: 860731; NID: 9408994; PIDN: AAC60441.1; PID: 9408996
R; Fauji, T.; Lida, T.; Honda, T.; Miwatani, T.; Nagahama, M.; Sakurai, J.; Wada, K. = Microb. Pathog. 2, 381-390, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Ibrahimi, I.; Gentz, R.
J. Biol. Chem. 262, 10189-10194, 1987
A;Title: A functional interaction between the signal peptide and the translation ap;==
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M17101; NID:g146375; PIDN:AAA23973.1; PID:g146376
R;Inoue, T.; Tsuji, T.; Koto, M.; Imamura, S.; Miyama, A.
FEMS Microbiol. Lett. 108, 157-161, 1993
A;Title: Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the A chain, whi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: A unique amino acid sequence of the B subunit of a heat-labile enterotoxin A;Reference number: A61475; WUD:89180953
A;Accession: A61475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: protein
A;Residues: 22-24,'S',26-27,'E',29-63,'K',65-66,'A',68-95,'A',97-122,'E',124 <TSU>
A;Experimental source: strain 240-3
                                                                                                 C;Species: Escherichia coli
C;Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change 18-Jun-1999
C;Accession: A01820; B26946; 141194; 141287; 167644; A61475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;22-124/Product: heat-labile enterotoxin chain B #status predicted <MAT>F;30-107/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the toxin is produced by
                                                                 heat-labile enterotoxin chain B precursor - Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: 141287; MUID:87280041
A;Accession: 141287
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: 153542; MUID:9325225
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F;1-21/Domain: signal sequence #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-22 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
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100.0%; Score 39; DB 100.0%; Pred. No. 0.3 ive 0; Mismatches Conservative Ouery Match Best Local Similarity Mismatches

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Pred. No. 0.38;

100.0%; Score 39; 100.0%; Pred. No. ( ó

Conservative

Best Local Similarity Matches 7; Conserv

Query Match

EVPGSQH 78 1 EVPGSQH 7

72

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Gaps

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0.38;

Length 124; Indels

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hypothetical protein - Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Species: Mycobacterium leprae
C; Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 26-May-2000
C; Accession: B27586
R: Booth, R.J.; Harris, D.P.; Love, J.M.; Watson, J.D.
J. Immunol. 140, 597-601, 1988
A;Title: Antiquenic proteins of Mycobacterium leprae. Complete sequence of the gene fo
A;Reference number: A92821; MUID:88088878
                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-455 -KUN>
A;Cross-references: GB:299105; GB:AL009126; NID:92632457; PIDN:CAB12043.1; PID:926325
A;Experimental source: strain 168
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C;Species: Caenonhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C;Accession: S44886
R;Du, Z.
Submitted to the EMBL Data Library, May 1993
A;Description: Sequence of the C. elegans cosmid ZK112.
A;Reference number: $44616
A;Accession: S44886
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 25/3; 65/2; 196/2; 249/1; 275/1; 385/2; 415/2
C;Superfamily: Caenorhabditis elegans ZK688.6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 1;
Pred. No. 48;
1; Mismatches
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57:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: ycbF
C;Superfamily: glucarate dehydratase
C;Keywords: carbon-oxygen lyase; hydro-lyase
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Pred. No.
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71.4%;
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Best Local Similarity 71.*.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-534 <DUZ>
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64 EVPGGEH 70
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S44886
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Whaternate names: Nto16 protein

Cispecies: Nicotiana tabacum (common tobacco)

Cispecies: Nicotiana (missecon tobacco)

Ry Tanaka-Ueguchi, M.; Itoh, H.; Oyama, N.; Koshioka, M.; Matsuoka, M.

Ry Tanaka-Ueguchi, M.; Itoh, H.; Oyama, N.; Koshioka, M.; Matsuoka, M.

Ry Tanaka-Ueguchi, M.; Itoh, H.; Oyama, N.; Koshioka, M.; Matsuoka, M.

A.; Reference number: Z14418

A.; Reference number: Z14418

A.; Accession: T01751

A.; Accession: T01751

A.; Accession: T01751

A.; Molecule type: mRNA

A.; Residues: 1-367 cTAN>

A.; Coss references: EMBL: AB016084

C; Genetics:
A.; Coss references: EMBL: Abortopane-1-carboxylate oxidase
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C;Species: Bacillus subtilis
C;Species: Do-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: A69753
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
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                                                                                                                                                                             Species: Homo sapiens (man)
Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
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                                                                                                                                         hypothetical protein DKF2p564A0122.1 - human
C;Species: Homo sapiens (man)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-
C;Accession: T14755
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
Submitted to the Protein Sequence Database, August 1999
A;Reference number: 218181
A;Accession: T14755
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-272 <WAM>
A;Cross-references: EMBL:AL110209
A;Experimental source: fetal brain; clone DKF2p564A0122
C;Genetics:
A;Note: DKF2p564A0122.1
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17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 2
Pred. No. 17;
2; Mismatches
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85.7%; Pred. No. 23;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.6%;
71.4%;
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Best Local Similarity 71.4*
Thes 5; Conservative
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246 ELPGSEH 252
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149 EVPSSQH 155
          EVPGSQH 78
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                                72
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C; Accession: G84533
R; Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
F, Leithauser, B.; Kellari, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. Us.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A; Freference number: A84160; MUID:20504483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C. Species: Deinococcus radiodurans
C. Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
C. Accession: H75446
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Beauchemin, M.; Savard, P.
Dev. Biol. 154, 55-65, 1992
A;Tile: Two distal-less related homeobox-containing genes expressed in regeneration
A;Reference number: A48820; MUID:93050784
A;Recession: B48820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A. Cross-references: GB:X63531; GB:S47223; NID:g432377; PIDN:CAA45094.1; PID:g432378
A:NOte: sequence extracted from NCBI backbone (NCBIN:117052, NCBIP:117053)
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Reywords: DNA binding; homeobox; nucleus; transcription regulation
F;126-182/Domain: homeobox homology <HOX>
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                                                                                                                                                                                                                                                                                      homeobox protein (clone NvHBox-4) - eastern newt
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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H75446
(S)-2-hydroxy-acid oxidase - Deinococcus radiodurans (strain R1)
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Pred. No. 45;
1; Mismatches
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71.4%;
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71.48;
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Best Local Similarity 71...
5; Conservative
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A; Residues: 1-273 <BEA>
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A:Molecule type: DNA
A:Residues: 1-274 <STO>
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Best Local Similarity
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                                                      :111 11
66 KVPGKQH 72
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            EVPGSQH
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C96827
C;Accession: C96827
C;Accession: C76827
C;Accessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C: Species: Streptomyces coelisolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
R:Aucression: T34767
R:Reference number: 221556
A:Reference number: 221556
A:Residues: 1-242
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C;Genetics:
A;Residues: 1-137 <BOO>
A;Cross-references: GB:M19058; NID:g149919; PIDN:AAA88230.1; PID:g1196505
C;Superfamily: Mycobacterium leprae hypothetical 15.2K protein
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Pred. No. 22;
1; Mismatches
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Pred. No. 4
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71.4%;
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83.3%;
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Best Local Similarity 83.3
Matches 5; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
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5; Conservative
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A; Residues: 1-260 <STO>
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205 EVPGTDH 211
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Best Local S
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N'Alternate names: ARP-1 protein; COUP-TFII
C;Specias: Mus musculus (house mouse)
C;Specias: Mus musculus (house mouse)
C;Date: O2-Jul-1996 #sequence_revision O2-Jul-1996 #text_change 20-Sep-1999
C;Accession: I48975; I48732; S44284
R;Oiu, Y; Cooney, A.J.; Kurstani, S.; DeMayo, F.J.; Tsai, S.Y.; Tsai, M.J.
Proc. Natl. Acad. Sci. U.S. A. 91, 4451-4455, 1994
A;Title: Spatiotemporal expression patterns of chicken ovalbumin upstream promoter-tr
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R;Jonk, L,J.; de Jonge, M.E.; Pals, C.E.; Wissink, S.; Vervaart, J.M.; Schoorlemmer, Mech. Dov. 47, 81-97, 1994
Mech. Dov. 47, 81-97, 1994
A;Title: Cloning and expression during development of three murine members of the COU A;Reference number: 148305; MUID:95034311
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                                                                                                                                                                                                                                                                                                                   protein homology
factor; zinc finge
Gene Expr. 1, 207-216, 1991
A;Title: The COUP-TFS compose a family of functionally related transcription factors.
A;Reference number: I54072; MUID:92314709
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C;Superfamily: unassigned erbA-related proteins; erbA transforming protein homology
C;Keywords: zinc finger
F;77-323/Domain: erbA transforming protein homology <ERBA>
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A;Molecule type: mRNA
A;Residues: 1-35,'P',37-414 <RE2>
A;Cross-references: EMBL:X76653; NID:9482927; PIDN:CAA54096.1; PID:9482928
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A,Map position: 15526.1-15526.2
C;Superfamily: unassigned erbA-related proteins; erbA transforming C;Keywords: DNA binding; lipid binding; lipoprotein; transcription F;77-323/Domain: erbA transforming protein homology <ERBA>
F;79-99/Region: zinc finger
F;115-139/Region: zinc finger
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A;Molecule type: mRNA
A;Residues: 1-414 <RES>
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100.0%; Pred. No. 71;
:ive 0; Mismatches
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Pred. No. 71;
0; Mismatches
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A; Accession: 148975
                                                                                                       A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-351 <RES>
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100.0%; Pre
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Matches 6; Conserv
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                                                                            A;Title: Genome Sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
A;Accession: H75446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-353 <WHI>A;Residues: 1-353 <WHI>A;Residues: 1-353 <WHI>A;Residues: 1-353 <WHI>A;Residues: 1-353 <WHI>A;Residues: C68:AE001954; GB:AE000513; NID:g6458751; PIDN:AAF10604.1; PID:g645875
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A;Reference number: A81500; MUID:20150255
A;Reference number: D83715
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-374 <TET>
A;Cross-references: GB:AE002300; GB:AE002160; NID:g7190365; PIDN:AAF39192.1; PID:g719037
A;Cross-references: GB:AE002300; GB:AE002160; NID:g7190365; A;Genetics:
A;Genetics:
A;Gene: TC0328
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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
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  , M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein TC0328 [imported] - Chlamydia muridarum (strain Nigg) C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000 C;Accession: D81715
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C;Superfamily: (S)-2-hydroxy-acid oxidase; (S)-2-hydroxy-acid oxidase homology
F;3-297/Domain: (S)-2-hydroxy-acid oxidase homology <2HY>
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A;Residues: 1-414 CADD-
A;Cross-references: GB:M64497; NID:g179023; PIDN:AAA86429.1; PID:g179024
R;Wang, L.H.; Ing, N.H.; Tsai, S.Y.; O'Malley, B.W.; Tsai, M.J.
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Science 251, 561-565, 1991
A;Title: Regulation of the apolipoprotein AI gene by ARP-1, a novel
A;Reference number: A37133; MUID:91118002
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Pred. No. 6
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Pred. No.
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Similarity 83.3%;
5; Conservative
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83.3%;
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Best Local Similarity 83.3'
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Best Local Similarity
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327 LPGSQH 332
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A; Molecule type: mRNA
A; Residues: 1-459 <CGO>
A; Residues: 1-459 <CGO>
A; Cross-references: GB: M29697; NID: g198377; PIDN: AAA39304.1; PID: g309411
A; Cross-references: GB: M29697; NID: g198377; PIDN: AAA39304.1; PID: g309411
R; Pleiman, C.M.; Gimpel, S.D.; Park, L.S.; Harada, H.; Taniguchi, T.; Ziegler, S.F.
Mol. Cell. Biol. 11, 3052-3059, 1991
A; Pleiman, C.M.; Gimpel, S.D.; Park, D.S.; Harada, H.; Taniguchi, T.; Ziegler, S.F.
A; A; Reference number: A40256; MUID: 91246172
A; Accession: C40256
Cell 60, 941-951, 1990
A; Title: Cloning of the human and murine interleukin-7 receptors: demonstration of a A; Reference number: A34791; MUID:90199875
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A;Cross-references: EMBL:282062; PIDN:CABO4890.1; GSPDB:GN00019; CESP:W02A11.3
A;Experimental source: clone W02A11
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A.Residues: 231-239,264-272 <PLE>
A.Residues: 21-239,264-272 <PLE>
C.Superfamily: interleukin-7 receptor; fibronectin type III repeat homology
C.Superfamily: interleukin-7 receptor; phosphoprotein; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-459/Product: interleukin-7 receptor #status predicted <MAT>
F;21-239/Domain: extracellular #status predicted <EXT>
F;240-264/Domain: transmembrane #status predicted <TWM>
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C;Accession: T26069
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Pred. No. 85;
1; Mismatches
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C;Superfamily: RING finger homology
F;429-479/Domain: RING finger homology <RRN>
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Pred. No.
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85.7%;
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Matches 6; Conserv
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                      N;Contains: chorismate synthase (EC 4.6.1.4); flavin reductase, NADPH-dependent C;Species: Neurospora crassa C;Date: 17-Mar-2000 #text_change 02-Sep-2000 C;Accession: T46725 R;Henstrand, J.M.; Amrhein, N.; Schmid, J. J. Balol. Chem. 270, 20447-20452, 1995 A;Ttle: Cloning and Characterization of a Heterologously Expressed Bifunctional Chorism A;Reference number: 206450; MUID:95386486 A;Accession: T46725 
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 23-Jul-1999
C;Accession: D34791; C40256
R;Goodwin, R.G.; Friend, D.; Ziegler, S.F.; Jerzy, R.; Falk, B.A.; Gimpel, S.; Cosman,
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Pred. No. 74;
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Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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Query Match Matches

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C;Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology F;237-294/Domain: immunoglobulin homology <IMM>
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. (C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Aritles Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: A96719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C. Accession: A43425
R; Kayyem, J.F.; Roman, J.M.; de la Rosa, E.J.; Schwarz, U.; Dreyer, W.J.
J. Cell Biol. 118, 1259-1270, 1992
A; Title: Bravo/Nr-CAM is closely related to the cell adhesion molecules L1 and Ng-CAM is A; Reference number: A43425, MUID:92381110
A; Scates preliminary; not compared with conceptual translation
A; Molecule type: nucleic acid; protein
A; Molecule type: cerebellum
A; Residues: 1-1259 cKAY>
A; Experimental source: cerebellum
A; Note: sequence extracted from NCBI backbone (NCBIP:112026)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted to the EMBL Data Library, March 1995
A; Description: The sequence of C. elegans cosmid B0228.
A; Description: The sequence of C. elegans cosmid B0228.
A; Reference number: 218324
A; Accession: T29041
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-1258 < LEI>
A; Residues: 1-1258 < LEI>
A; Cross-references: EMBL; U23168; PIDN: AAC38813.1; CESP: B0228.4
A; Experimental source: strain Bristol N2
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: 299/2; 393/3; 435/1; 586/1; 615/3; 655/3; 678/3; 701/3; 1213/3
C; Superfamily: Caenorhabditis elegans hypothetical protein B0228.4
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                                                                                                                                                                                                                             A;Molecule type: DNA A;Rolecule type: DNA A;Residues: 1-1028 <STO> A;Cross-references: GB:AE005173; NID:g6665545; PIDN:AAF22914.1; GSPDB:GN00141 C;Genetics:
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Bravo/Nr-CAM cell adhesion molecule L1 homolog - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Caenorhabditis elegans
Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
Accession: T29041
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Pred. No. 2.3e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 2; Length 1028;
Pred. No. 1.9e+02;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein B0228.4 - Caenorhabditis elegans
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85.7%;
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illarity 83.3%;
Conservative
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Best Local Similarity 85.7%
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Best Local Similarity
Matches 5; Conserv
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| 195 EVPGSIH 201
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636 VPGSEH 641
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R; Leimbach, D.
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R; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. A; Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A; Reference number: A72450; MUID:99310339
A; Rocesion: B72782
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-148 <KAW>
A;Cross-references: DDBJ:AP000058; NID:g5103388; PIDN:BAA79156.1; PID:d1042932; PID:g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-153 <WAT>
A; Cross-references: EMBL: AF016416; PIDN: AAB65273.1; GSPDB:GN00020; CESP:F29A7.3
A; Experimental source: strain Bristol N2; clone F29A7
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C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C; Accession: T31701
A; Description: The sequence of C. elegans cosmid F29A7.
A; Reference number: 221071
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                               C.Species: Aeropyrum pernix
C.Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C.Accession: B72782
                                                    Gaps
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    Length 1259;
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                                               0; Indels
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C;Superfamily: Aeropyrum pernix hypothetical protein APE0243
                                                                                                                                                                                                                                                         hypothetical protein APE0243 - Aeropyrum pernix (strain K1)
79.5%; Score 31; DB 2; L
100.0%; Pred. No. 2.3e+02;
iive 0; Mismatches 0;
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Pred. No. 39;
0; Mismatches
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Pred. No. 40;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T6.9%; Sc. Similarity 100.0%; P. 5; Conservative 0;
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71.4%;
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                                                 6; Conservative
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Best Local Similarity 71.4
Matches 5; Conservative
    Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
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| EVPGSQ 656
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Conserved hypothetical protein PA0054 [imported] - Pseudomonas aeruginosa (strain PA01) Conserved hypothetical protein PA0054 [imported] - Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa C; Species: Dseudomonas aeruginosa C; Species: Dseudomonas aeruginosa C; Species: Dseudomonas aeruginosa S; September: Dseudomonas aeruginosa S; Van, Y. Palam, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yaun, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Jacry, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Tile: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A; Reference number: A82950; MUID: 20437337
A;Accession: D83638
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-182 cSTO-A;CSTO-A;CSS-references: GB:AE004445; GB:AE004091; NID:99945872; PIDN:AAG03444.1; GSPDB:GN001
C;Genetics: A;Gene: PA0054
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Pred. No. 48;
1; Mismatches 0; Indels
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Best Local Similarity 83.3%;
Matches 5; Conservative
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Search completed: July 16, 2001, 16:37:00 Job time: 209 sec

2 VPGSQH 7 ||||:| 118 VPGSRH 123

g ç

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 16, 2001, 16:35:46; search time 57.41 Seconds

(without alignments)

16.132 Million cell updates/sec

Title: US-09-786-648-2

Sequence: 1 EVPGSQH 7

Scoring table: BLOSUM62

Gappp 10.0, Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	O9r646 vibrio chol	057193 vibrio chol	vibrio		022511 vitis vinit	09w7d3 orvzias lat	09w7d4 orvzias lat	O9r1z8 streptomyce	Ognod Spoie	09uq04 homo sapien	080418 nicotiana	Q9y2b3 homo sapien	Q9vfe2 drosophila	Q9fqi8 amaranthus	O70284 mus musculu	09fqi8 amaranthus	O9w2v0 drosophila	Q91195 mus musculu	086582 streptomyce	
	ΙD	Q9R646	057193	056635	Q9RP15	022511	Q9W7D3	09W7D4	Q9RJZ8	904N60	Q90G04	080418	Q9Y2B3	Q9VFE2	Q9FQI8	070284	Q9FQJ8	Q9W2V0	Q9JL95	086582	
	DB	5	7	7	~	10	13	13	7	4	4	10	4	S	10	11	10	Ŋ	11	7	
	Query Match Length DB	103	124	124	124	565	195	199	201	192	272	367	412	898	95	765	95	122	222	242	
dР	Query Match	100.0	100.0	100.0	100.0	89.7	87.2	87.2	87.2	84.6	84.6	84.6	84.6	84.6	82.1	82.1	79.5	79.5	79.5	79.5	
	Score	39	39	39	39	35	34	34	34	33	33	33	33	33	32	32	31	31	31	31	
,	Result No.	-	7	ю	4	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	,

Q99y63 m:ns musculu Q9ma16 arabidopsis 29hmm5 halobacteri O16391 drosophila Q9rvj7 deinococcus Q9rvj7 chiamydia m Q9v7m7 chiamydia m Q9v7m7 chiamydia m Q9y7m7 chiamydia m Q9y001 mus musculu Q91if8 arabidopsis Q9xum8 caenorhabdi Q9num8 caenorhabdi Q9m4h3 vitis vinif Q9m4h3 vitis vinif Q9m4h3 vitis vinif Q9m4h3 vitis vinif Q9yfk5 acropyrum p Q16208 caenorhabdi Q9yfk5 acropyras lat	
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## ALIGNMENTS

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ae; Vibrio.	cholerae	103; s 0; Gaps 0;	
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PRT; 103 AA. Created) Last sequence update) Last annotation updat SUBUNIT. amma subdivision; Vibr	0; ne N.; oxin produ 95).	Score 39; D Pred. No. 0. Mismatches	PRT; 124 AA. 01, Created) 1. Last sequence update) 15, Last annotation update) (CTB) PRECURSOR (CTB)
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998646 PRELIMINARY; 098646; 01-MAY-2000 (TrEMBLrel. 13 01-MAY-2000 (TrEMBLrel. 13 01-OCT-2000 (TrEMBLrel. 15 CHOLERA-LIKE ENTEROTOXIN B Bacteria; Proteobacteria; e NCBI_TRAID-666;	SEQUENCE.  MEDLINE-95303036; Pubme Nakashima K., Eguchi Y.  "Characterization of an 0139."; P0156; IXTC.  HSSP: P0156; IXTC.  InterPro: IPR001835; -  Pfam; PF01376; Enteroto PRINTS; PR00172; ENTERO	Query Match Best Local Similarity Matches 7; Conser' 1 EVPGSQH 7 1 IIIIII	2 57193 57193; 57193; 1-NOV-1996 1-OCT-2000 HOLERA TOXI
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Indels

Length 124;

DB 2; 0.86;

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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID-666;
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STRAIN=KNIH002;
Shin H.J., Park Y.C., Kim Y.C.;
Shin H.J., Park Y.C., Kim Y.C.;
Shin H.J., Park Y.C., Kim Y.C.;
Shin H.J., Park Y.C.,
Cassette from Vibrio cholerae KNIH002 isolated in Korea.";
Misalimurhag Hoiji 35.205-210(1999).
EMBL; AF175708; AAD51360.1; -..
HSSP: P01556; 2CHB.
124 AA; 13871 MW; 3F87B2F297953179 CRC64;
                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERS ENTEROTOXIN B-SUBUNIT.
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                                          100.0%; Score 39; 100.0%; Pred. No.
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Mendel; 26381; Vitvi;1190;26381.
InterPro; IPR000103; -
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                                          Query Match 100.
Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity 100.
Matches 7; Conservative
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SEQUENCE FROM N.A.
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                                                                     "Comparison of cholera toxin genes (ctxAB) of non-Ol vibrio cholerae strains 854 (0139-bengal) and 87 (037) from two outbreaks."; Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases. EMBL; D30052; BAA06289.1; -. HSSP; P01556; 2CHB.
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               Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
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NCBL_raxID=666;
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Yamamoto K., Do V.G., Xu M., Iida T., Miwatani T., Albert M.J.,
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D6BF83FFF7924EA3 CRC64;
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Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X58785; CAA41591.1; -.
EMBL; W256795 AAC34728.1; -.
EMBL; A00931; CAA00098.1; -.
HSSP; P01556; 2CHB.
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Last sequence update)
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Shi C., Cao C., Zhang J., Ma Q.;
Chin. Blochem. J. 9:395-399(1993).
                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001835; -.
Pfam; PF001376; EnterOttoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
Probom; PD012805; -; 1.
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22 124 C
124 AA; 13919 MW;
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Best Local Similarity 100.

Matches 7; Conservative
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72 EVPGSQH 78
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Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; Vitis.
NCBI_TaxID=29760;
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SEQUENCE FROM N.A.
STATAIN-CV. THOMBOON SEEDLESS (CLONE 2A); TISSUE-FRUIT;...
Cassol T., Adams D.O.
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: FAD (BY SIMILARITY).
-!- SIMILARITY: TO PYRIDINE NUCLEOTIDE-DISULPHIDE OXIDOREDUCTASES CLASS-I.
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                                                                                                                                                                                      Length 124;
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InterPro; IPR001835; -.
Pfam; PF01376; EnterProtoxin_B; 1.
PRINTS; PR00772; ENTERCOTOXINB.
SEQUENCE 124 AA; 13905 WW; 23BF83FFF793E5B9 CRC64;
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01-JAN-1998 (TREMBLrel. 05, Last sequence update)
01-JAR-2091 (TrEMBLrel. 16, Last annotation update)
GLUTARH-2001 (TrEMBLrel. 16, Last annotation update)
GLUTATHIONE REDUCTASE (NADPH) (EC 1.6.4.2) (FRAGMENT).
                                                                                                                                                                                  100.0%; Score 39; DB 2; 100.0%; Pred. No. 0.86;
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15.1

Gaps

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Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;

*A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

EMBL; AL132210; CAB61584.1; -.

Interpro; IPR002502; -.

Pfam; PF01510; Amidase_2; 1.

SEQUENCE 201 AA; 22749 MW; B8EF477E06A20468 CRC64;
  Kanamori A.; "Systematic identification of genes expressed during early obgenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor.
Bacteria; Firmioutes; Actinobacteria; Actinomycetales; Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1902;
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100.0%; Pred. No. 16;
tive 0; Mismatches 0; Indels
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85.7%; Pred. No. 16;
vative 0; Mismatches 1; Indels
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oliver K., Harris D.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                  in medaka.";
Mol. Reprod. Dev. 0:0-0(1999).
EMBL. AF128817. AAD38914.1; -.
Hypothetical protein.
SEQUENCE 199 AA, 21726 MW; E9827C05451B15CD CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
LLPL, LCAT-LIKE LYSOPHOSPHOLIPASE (FRAGMENY).
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                                                                                                                                                                                                                                          Query Match 87.2
Best Local Similarity 100.
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 13, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last an
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                                                                                                                                                                                                                                                                                                                     89.7%; Score 35; DB 10; Length 565; 71.4%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                Indels
                PERMIS PRO070; pyr_redox; 1.
PRINTS: PRO041; PADPARABEL.
PRINTS: PRO0469; PUDRDTARBEL.
PROSITE; PRO0469; PUREDINE_REDOX_1; 1.
FAD; FAUPOPROPEIN; OXIGOREGICASE; PARIOPROFIN; PARIOREREDOX_1; 1.

NON_TER.
1 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mol. Reprod. Dev. 0:0-0(1999).
EMBL: AF128818; AAD38915.1; -.
Hypothetical protein.
SEQUENCE 195 AA; 21446 MW; B90682D695729E88 CRC64;
                                                                                                                                                                                                                                       SEQUENCE 565 AA; 60695 MW; B26113AE09A121DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O. Created)
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHERICAL 21.7 KDA PROTEIN.
Oryzias latipes (Medaka fish).
                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 199 AA
                                                                                                                                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                        Query Match 89.7
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
InterPro; IPR001100; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=ORANGE-RED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-ORANGE-RED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|||:|
239 EIPGSEH 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8090;
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                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VPGSQH 7
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Q9W7D4;
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Q9W7D3;
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RESULT Q9W7D3

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Gaps

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RESULT Q9W7D4

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Gaps

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Length 367;

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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;
                                                                                                                                   Tanaka-Ueguchi M., Itoh H., Oyama N., Koshioka M., Matsuoka M., "Over-expression of a tobacco homeobox gene, NTH15, decreases the expression of a gibberellin biosynthetic gene encoding GA 20-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-99194552: PubMed-10092508;
Taniyama Y., Shibata S., Kita S., Horikoshi K., Shirafuji H., Sumino Y., Fujino M.;
Sumino Y., Fujino M.;
"Cloning and expression of a novel lysophospholipase which structurally resembles lecithin cholesterol acyltransferase.";
Blochem Biophys. Res. Commun. 257:50-56(1999).
InterProj. IPR003386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09VFE2:
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CG3837 PROTEIN.
GC3837.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.6%; Score 33; DB 4; Length 412; ilarity 71.4%; Pred. No. 53; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                 Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB016084; BaA31690.1; -.
Mendel; 31081. Nicta;2972;31081.
InterPro; IPR002419; -.
                                                                                                                                                                                                                                                                                           Pfam; PF00671; Fe_Asc_oxidored; 1.
SEQUENCE 367 AA; 42170 MW; 923BC90B3BBBAC05 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02450; LACT; 1.
SEQUENCE 412 AA; 46657 MW; 1FEA8A5783AF050A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 10;
Pred. No. 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       412 AA
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                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         84.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCAT-LIKE PROTEIN (LLPL).
                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 EVPSSQH 155
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386 ELPGSEH 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVPGSQH 7
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                                                                                                                                                                                                 oxidase.
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                                                                                                                                                                                                               Auffray C., Ansorge W., Ballabio A., Estivill X., Gibson K.,
Lehrach H., Poustka A., Lundeberg J.;
"The European IMAGE consortium for integrated Molecular analysis of
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN;
Wambutt R., Heubner D., Mewes H.W., Gassenhuber J., Wiemann S.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ALI10209; CAB53675.1; -.
InterPro: IPR003386; -.
Pfam: PF02450; LACT; 1.
Hypothetical protein.
SEQUENCE 272 AA; 31016 MW; ACCC5E1680D7A720 CRC64;
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Pred. No. 24;
2; Mismatches 0; Indels
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Pred. No. 35;
2; Mismatches 0; Indels
                                                                                                                   SEQUENCE FROM N.A. Pluvinet R., Sumoy L.; Sluvinet R., Estivill X., Escarceller M., Sumoy L.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                     human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL389957;
OND TER
SEQUENCE 192 AA; 21609 MW; 04A7AE8CB344F213 CRC64;
                                                                                                                                                                                                                                                                                                                                                     192 AA; 21609 MW; 04A7AE8CB344F213 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETCAL 31.0 KDA PROTEIN.
DKF2P564A0122.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.6%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                           84.6%;
71.4%;
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Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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166 ELPGSEH 172
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246 ELPGSEH 252
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RESULT 10 Q9UG04 **090G04** 

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RESULT 11 080418 ID 080418 AC 080418 DT 01-NOV DT 01-NOV DT 01-JUN DT 01-JUN DT 01-JUN ON NTC16 GN NTC16

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                                                                                                                                                              Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F., Gocayne G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X., Radadon R.C., Nogers Y.-H.C., Blazej R.G., Champen M., Pfeiffer B.D., Radadon R.C., Maklos G.L.G., Mannen B.L., Baucher E.G., Helt G., Nelson C.R., Miklos G.L.G., Maril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D., Ballews R.W., Basus R.Y., Banca P.P., Bhandari D., Blashakov S., Borthan M.R., Bouchen M.R., Bultler H., Caddeu E., Center A., Chandra I., Burtls R.C., Busam D.A., Bultler H., Caddeu E., Center A., Chandra I., Radoson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Radoson K., Cabrielian A., Carle G.C., Ferraz C., Ferraz 
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TREMBLSELIKE PROTEIN (FRAGMENT)
Amaranthus quitenensis.
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  868 AA; 98349 MW; F6562A64E72E7B21 CRC64;
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                                                                                                                             STRAIN-BERKELEY;
MEDLINE-20196006; PubMed=10731132;
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Pfam; PF01030; 'Recep_L_domain; 2.
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003706; AAF55118.1; -. FlyBase; FBgn0038279; CG3837.
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                                                                                                  SEQUENCE FROM N.A.
                        Ephydroidea; Dros
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:||:||
812 ELPGTOH 818
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Q9FQI8;
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Q9FQI8
OOC KEENER KEENE
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Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97020303; PubMed-8812055; MEDLINE-97020303; PubMed-8812055; Kuwana E., Bulfone A., Fletcher C.F., Copeland N.G., Jenkins N.A., Crews S., Martinez S., Puelles L., Rubenstein J.L., Tessier-Lavigne M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ő
Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae;
Caryophyllales; Amaranthaceae; Amaranthus.
NCBI_TaxID=107609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Expression patterns of two murine homologs of Drosophila minded suggest possible roles in embryonic patterning and pathogenesis of Down syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                       Score 32; DB 10; Length 95;
Pred. No. 20;
1; Mismatches 1; Indels
                                                                                                                                                                                                    retrotransposons in plants.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF232993; AAG44333.1;
                                                                                                                                                      He Y., Sun M.; "Reverse transcriptase sequence evolution in copia-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     May N.R., Fan C.-M.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AF038857; AACO5481.1; -
EMBL: AF044913; AACO5481.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAC; 1.
AA; 85575 MW; 46AC6BFD8A189126 CRC64;
                                                                                                                                                                                                                                                                                                                      95 AA; 11392 MW; 8E931447E1683C5C CRC64;
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Last annotation update)
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Pred. No. 1.6e+02;
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                                                                                                                                TRANSPOSON-COPIA-LIKE RETROTRANSPOSON;
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EMBL, AF038854; AAC05481.1; JOINED
EMBL; AF038855; AAC05481.1; JOINED
EMBL; AF038855; AAC05481.1; JOINED
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00785; PAC; 1.
Pfam; PF00989; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001092;
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Best Local Similarity
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                                                                                                          SEQUENCE FROM N.A.
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SEQUENCE 765 A
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26 EVPGKEH 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVPGSQH 7
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                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Best Local Similarity
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A MADINE-20196006; PubMed=10731132;

A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

A Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champen M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Beson K.M., Benoss P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA George S., Dahlke C., Davenport L.B., Davies P.,

RA George R.A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Medazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                              Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Amaranthaceae; Amaranthus.
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 10; Length 95;
Pred. No. 32;
2; Mismatches 1; Indels
 Indels
                                                                                                                                                                                                                                                                                 He Y., Sun M.; Reverse transcriptase sequence evolution in copia-like retrotransposons in plants."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF232981; AAG44323.1; -...
                                                                                                                                                                                                                                                                                                                                                                      95 AA; 11241 MW; 36403CBDC40D769A CRC64;
                                                                                                                                               Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence upda
01-MAR-2001 (TrEMBLrel. 16, Last annotation up
01-MAR-2001 (TrEMBLRel. 16, Last annotation up
Amaranthus quitensis.
                                                                                                            95 AA.
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 Mismatches
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TRANSPOSON-COPIA-LIKE RETROTRANSPOSON;
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-MAY-2000 (TrEMBLrel. 13, Last ann
CG15303 PROTEIN.
                                                                                                            PRT;
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57.1%;
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Best Local Similarity 57.1
Matches 4; Conservative
6; Conservative
                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                    NCBI_TaxID=107609;
                                       423 ERPGSQH 429
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26 EIPGKEH 32
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                     1 EVPGSQH 7
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NON_TER
SEQUENCE
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                                                                                   RESULT 16
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Matches
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Gaps
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J. Leukoc. Biol. 0:0-0(2000).
EMBL; AF20253; AAF26366.1; -.
InterPro; IPR001304; -.
InterPro; IPR002352; -.
Prims; PR0059; Lectin_c; 1.
PRINTS; PR00770; EMAJORBASICP.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-C57BL/6J; TISSUE-BONE MARROW;
Macias M.P., Welch K.C., Denzler K.L., Larson K.A., Lee N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0030203; CG15303.
SEQUENCE 122 AA; 13139 MW; EF8D5468CFDE88E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25204 MW; 1A28C69888FC52FF CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
EOSINOPHIL MAJOR BASIC PROTEIN 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79.5%; Score 31; DB 71.4%; Pred. No. 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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SEQUENCE FROM N.A.
STATEL/6J; TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 71.4
Matches 5; Conservative
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25 EAPGSRH 31
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Length 222;

DB 11; 75;

Score 31; Pred. No.

79.5%; 85.7%;

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12 VPGAQH 17
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                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; ALO31184; CAA20190.1;
InterPro: IPR005202;
Pfam; PF01510; Amidase_2; 1.
Hypothetical protein.
  Gaps
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
INTERLEUKIN-1 RECEPTOR ASSOCIATED PROTEIN KINASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.5%; Score 31; DB 2; Length 242; 71.4%; Pred. No. 81;
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy L., Harris D.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26018 MW; 6DD10FF18A2EC544 CRC64;
                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAX-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL 26.0 KDA PROTEIN.
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1;
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Mismatches
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                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97000351; PubMed-8843436;
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Conservative
                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1902;
                                                                           61 EVEGSOH 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVPGSQH 7
                                   1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-A3(2);
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9
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                                                                                                                                                                             086582
086582;
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Matches
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Q9QY63
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DDT TDD TDD TDD TDD TDD TDD DDT DD
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SEQUENCE FROM N.A. Checks S., Buehler E., Chao Q., Johnson-Hopson C., Cheuk R., Shinn P., Brooks S., Buehler E., Chiou J., Choi E., Comen L., Conway A. Gonzalez A., Hansen N., Howing B., Koo T., Lem B., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic sequence for Arabidopsis thaliana BAC F20B17 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Khan S., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C.,
Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Ecker J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
and mouse reveals new untranslated sequences.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF121351; AAF22115.1; -.
MGD; MGI:107420; Illrak.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Theologis A., Ecker J.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO10793; AAF681106.1;
SEQUENCE 260 AA; 29128 WW; B149F22073AA0B92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ecker J.R.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                    ED22D000546F0E88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                          DB 11;
82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 AA
                                                                                                                                                                                                                                                       ATP-binding, Kinase, Receptor, Transferase.
NON_TER 243 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                         InterPro; IPR000719; -...
Pfam; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATF; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          Score 31;
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                    243 AA; 26539 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       79.5%;
nilarity 83.3%;
Conservative
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Best Local Similarity
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ZYGOTICALLY.
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305 EVPGTHH 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVPGSQH 7
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SEQUENCE
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MEDLINE-20504483; PubMed=11016950;
MGDLINE-20504483; PubMed=11016950;
MGDLINE-20504483; PubMed=11016950;
SWATKIE H.D., Lasky S.R., Ballga N.S., Thorsson V., Sbrogna J.,
SWATKIEL S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Danniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99051329, PubMed-9831651;
Chan H.Y.E., Harris S.J., O'Kane C.J.;
"Identification and characterization of kraken, a gene encoding
putative hydrolytic enzyme in Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79.5%; Score 31; DB 1; Length 274; 71.4%; Pred. No. 92; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                      Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-37N-1998 (TrEMBLrel. 05, Created)
01-3AN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PROBABLE SERINE HYDROLASE (EC 3.1.-.-) (KRAKEN PROTEIN).
KRAKEN OR CG3943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
EMBL; AE005096; AAG20195.1; -.
SEQUENCE 274 AA; 29944 MW; 2BE706911A76CD3D CRC64;
                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                           1-MAR-2001 (TrEMBLrel. 16,
1-MAR-2001 (TrEMBLrel. 16,
1-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=64091;
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                        :111 ||
66 KVPGKOH 72
1 EVPGSQH 7
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                                                                                                                                                                                                                                                                                                                                                   Halobacterium
                                                                                                                                                                                              01-MAR-2001
01-MAR-2001
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01-JAN-
                                                                                                                                                   Q9HNM5
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1018391
10 018391
20 018391
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10 1-JAN

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RAMERICA G.C., Norens Y. H.C. Yanddil N.D., Thang O. Clear L.D.
RAMERICA G.C., Norens Y. H.C. Yanddil N.D., Thang O. C., Clear L.D.
RAMERICA G.C., Norens Y. H.C. C. Medica G. Neighbor M. Prelifer B.D.
RAMERICA G.C., Norens Y. H.C. C. Medica G.C., Balddil D.D.
RAMERICA G.C., Norens Y. H.C. Medica G.C., Balddil D.D., Rallew R.M., Beacon F.V., Berman B.P., Phandari D., Bolshakov S.,
RAMERICA G.C., Norens W.W., Berman B.P., Phandari D., Bolshakov S.,
RAMERICA G.C., Ranger B.C., Reference E.C., Ferrers G.C., Ferrers G.C
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                                                                                                                                                                                          STRAIN=R1;
MEDLINE=20036896; PubMed=10567266;
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Richardson D.L.,
Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
Yamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 41.6 KDA PROTEIN.
Zymomonas mobilis.
Bacteria; Proteobacteria; alpha subdivision; Sphingomonas group;
                                                                                                                        Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
NCBL_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lee J.S., Kang H.S.; "Sequence analysis of 65G3 cosmid clone of Zymomonas mobilis ZM4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 79.5%; Score 31; DB 2; Length 353; Best Local Similarity 83.3%; Pred. No. 1.2e+02; Matches 5; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.5%; Score 31; DB 2; Length 371; 83.3%; Pred. No. 1.3e+02; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      containing rrnå operon.";
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF0088914;
InterPro; IPR000139;
Probom; P005242; -; 1.
Hypothetical protein.
SEQUENCE 371 AA; 41559 MW; 8D519E1509BAB64F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INCELTO, FENCENCY, 1.
PROSITE; PS00557; FMN_HYDROXY_ACID_DH; 1.
SROHFNCE 353 AA; 37877 MW; 14FB78FAEZE18C8D CRC64;
                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2001 (TrEMBLrel. 16, Last annotation update)
(S)-2-HYDROXY-ACID OXIDASE.
353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 371 AA
PRT;
                                                                                                                                                                                                                                                                                                                                                                          Science 286:1571-1577(1999).
EMBL; AE001954; AAF10604.1;
HSSP; P05414; 1GOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 79.5
Best Local Similarity 83.3
Matches 5; Conservative
PRELIMINARY;
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                                                                                                              Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000262; -.
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                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 VPGSEH 194
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Q9RH15;
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DR1031
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Q9RH15
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Gaps

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288 LPGSQH 293
2 VPGSQH 7
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Search completed: July 16, 2001, 16:43:36 Job time: 470 sec

Sequence 23, 8 Sequence 30, 8 Sequence 133, 8 Sequence 13, 8 Sequence 1, M Sequence 35, 8 Sequence 35,

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APPLICANT: COCKLE, Stephen A.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COOMEN, Raymond P.
APPLICANT: LOSMORE, Sheena
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF DEBORES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBUINEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: M5G IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
US-08-209-521-23
US-08-209-521-30
US-08-961-810-133
US-08-961-810-133
US-08-952-902D-133
US-08-952-902D-133
US-09-073-354-1
US-09-073-359-1
US-09-133-259-1
US-09-1418-027-1
US-09-1418-027-1
US-08-96-925-4
US-08-96-925-4
US-08-96-925-4
US-08-955-125-83-12
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US-08-96-925-4
US-08-96-925-4
US-08-96-925-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-NAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-388
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,966
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 26, Application US/08292968 Patent No. 5856122 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            READ, Randy J.
STEIN, Penelope E.
COCKLE, Stephen A.
OOMEN, Raymond P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INPORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 93 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abbana Sura
STREET: Sura
CITY: Toronto
   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
   Patent No. 5223610
Sequence 2, Apply
                                                                                                                July 16, 2001, 16:36:18; Search time 30.3 Seconds (without alignments) 13.962 Million cell updates/sec
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Sequence 12,
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Sequence 4,
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Sequence 8
Sequence 2
Sequence 2
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-952-337-1
US-08-952-337-2
US-08-747-410-2
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US-08-467-976-26
US-09-082-514-26
US-09-082-514-26
US-08-952-337-5
US-08-952-337-6
US-08-952-337-6
US-08-972-171-2
US-09-074-297-2
US-09-374-526-2
US-09-374-526-2
US-09-374-597-2
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US-08-435-605A-12
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US-08-222-715B-27
US-08-709-784-2
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US-09-027-337-2
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US-09-272-796-2
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
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107
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Match
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APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COMEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: LOOSMORE, Sheena
APPLICANT: HAZES, Bart
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: SIM & MCBULNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 107; DB 2; Best Local Similarity 100.0%; Pred. No. 2.2e-11; Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                   STATE: Ontario
CONDURES:
COMPUTER: Canada
ZIP: M5G 187
COMPUTER: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DGORET NUMBER: 1038-455 MIS:vg
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                     Sequence 26, Application US/08467536 Patent No. 5977304
                     1 GETFQVEVPGSQHIDSQKKAI 21
                                                         35 GETFQVEVPGSQHIDSQKKAI 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35 GETFQVEVPGSQHIDSQKKAI 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                               GENERAL INFORMATION:
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US-08-467-536-26
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US-08-467-976-26
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                                                       Length 93;
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                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                           APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COCKLE, Stephen A.
APPLICANT: COMEN, Raymond P.
APPLICANT: LOOSMORE, Sheena
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: MISS, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBULDRY
STREET: SLILE 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,974
                                                       Score 107; DB 2;
Pred. No. 2.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,993
REFERENCE/DOCKET NUMBER: 1038-454 MIS:vg
TELECOMMUNICATION INFORMATION:
                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435

ROOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-7UN-1995
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
FILING DATE: 24-AUG-1993
ATTORNEY ARENT INFORMATION:
                                                                                                                                                                                                                                                                       Sequence 26, Application US/08467974 Patent No. 5965385 GENERAL INFORMATION:
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                                                       100.0%;
100.0%;
                                                                                                                                                         35 GETFOVEVPGSQHIDSQKKAI 55
                                                                                                                                     1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1153
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                     Query Match
Best Local Similarity 100.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
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Best Local Similarity
Matches 21; Conserve
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                                                                                                                                                                                                                                   RESULT 2
US-08-467-974-26
US-08-292-968-26
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GENERAL INFORMATION:
APPLICANT: Meinersmann, Richard J.
APPLICANT: Meinersmann, Richard J.
APPLICANT: Meinersmann, Richard J.
APPLICANT: Meinersmann, Campylobacter Jejuni Flagellin-Escherichia Coli LT-B Fusion NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
STREET: Room 411, Building 005, BARC-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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COUNTRY: USA
ZIP: 20705
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
TITING DATE: 18-AUG-1997
TITING DATE: 18-AUG-1997
                                                                                                                                                                                    CITY: TOTORIO
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1F7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC compatible
COMPUTER: TEM PC COMPUTER:
CLEASITION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,514
FILING DATE:
CLEASIFICATION
PRICE STEMATO:
PRICA APPLICATION NUMBER: US 08/292,968
FILING DATE:
APPLICATION NUMBER: US 08/292,968
FILING DATE:
APPLICATION NUMBER: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEMARY, Michael I.
RECISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-810
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                            APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 107; DB 4;
100.0%; Pred. No. 2.2e-11;
iive 0; Mismatches 0;
                                                                                                                        ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/08829026A Patent No. 5837825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
  APPLICANT: ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GETFQVEVPGSQHIDSQKKAI 21
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Best Local Similarity 100.0
Matches 21; Conservative
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US-08-829-026A-6
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                                                                                                                                                                                                                                                                      MODIFICATION OF PERTUSSIS TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 107; DB 3;
100.0%; Pred. No. 2.2e-11;
tive 0; Mismatches 0;
                                                             APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: OOMEN, Raymond P.
APPLICANT: LOCSWORE, Sheena
APPLICANT: LOCSWORE, Sheena
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBURDAY
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
CONTENT: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATIBLE STSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1038-453 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADPLICATION NUMBER: US/08/467,976
FILING DATE: 06-JUN-1995
CLASSIFRCATION: 435
FILOR APPLICATION BATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION NUMBER: US 08/251,121
FILING DATE: 24-AUG-1993
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Application US/09082514
Patent No. 6168928
GENERAL INFORMATION:
APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
Sequence 26, Application US/08467976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPAN: (416) 595-1155
TELEPAX: (416) 595-1153
INFORMATION FOR SEC ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 READ, Randy J.
STEIN, Penelope E.
COCKLE, Stephen A.
OOMEN, RAYMOND P.
KLEIN, Michel H.
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Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY:
US-08-467-976-26
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US-09-082-514-26
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Gaps

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GENERAL INFORMATION:
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: Tacobb, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 94.4%; Score 101; DB 3; L
Best Local Similarity 95.2%; Pred. No. 2.7e-10;
Matches 20; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Sim & McBurney
330 University Avenue, Suite 701
EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER FILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 102
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/08472171; Patent No. 5932714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 GATFQVEVPGSQHIDSQKKAI 64
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Best Local Similarity 95.2'
Matches 20; Conservative
                                                                                                                                                                                                                                              ; ORGANISM: Escherichia coli
US-08-952-337-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-472-171-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 330 Univ
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino
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APPLICANT: Holmgren, Jan

APPLICANT: Holmgren, Jan

APPLICANT: LOBENS, Michael R.

TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE

TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS

FILE REFERENCE: 3846/0D758

CURRENT APPLICATION NUMBER: US/08/952,337

CURRENT FILING DATE: 1998-01-05

EARLIER PILING DATE: 1996-05-02

EARLIER FILING DATE: 1996-05-05

EARLIER FILING DATE: 1996-05-05

SOFTWARE: FALSO ID NOS: 6

SOFTWARE: FALSEQ for Windows Version 3.0

FEARLIER PLICATION NUMBER: APPLICATION NUMBER: A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 371;
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APPLICANT: Holmgren, Jan
APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/0D758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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95.2%; Pred. No. 2.7e-10;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 107; 100.0%; Pred. No. 1
                                                                                                              0106.97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08952337 Patent No. 6019973
                                       NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 0106
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-504-5676
TELEFAX: 301-504-5060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                 TELEFAX: 301-504-5060
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 antho actids
                                                                                                                                                                                                                                                                                                                     : 371 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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CRGANISM: Vibrio cholerae
US-08-952-337-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 20; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 21; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-829-026A-6
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                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION DATA:
FILING DATE:
APPLICATION NUMBER:
CLASSIFICATION DATA:
FILING DATE:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
ATOMNEY AGENT, MICHAEL I.
REGISTRATION NUMBER:
REGISTRATION NUMBER:
TELECOMMUNICATION NUMBER:
TELECOMMUNICATION NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 101; DB 2;
Pred. No. 2.8e-10;
0; Mismatches 1.
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.4%; Scc.
95.2%; Prec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                            TELEFAX: 416-595-1163
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2
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US-09-374-597-2

Sequence 2, Application US/09374597

Patent No. 6140082

GENERAL INFORMATION:

APPLICANT: Loosmore, Sheena M.

APPLICANT: Yacoob, Reza K.

APPLICANT: Zealey, Gavin R.

APPLICANT: Riein, Michel H.

TITLE OF INVENTION: Expression Of Gene Products From

TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella

NUMBER OF SEQUENCES: 56

CORRESPONDENCE: Sim & MCBULNEY

STREET: 330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 103;
                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/374,597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 94.4%; Score 101; DB 2; Best Local Similarity 95.2%; Pred. No. 2.8e-10; Matches 20; Conservative 0; Mismatches 1.
                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/472,171
FILING DATE: 07-UNN-1995
PRIOR APPLICATION NUMBER: US 08/393,334
APPLICATION NUMBER: US 08/393,334
FILING DATE: 23-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/013,047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1153
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GETFQVEVPGSQHIDSQKKAI 21
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amino acid
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COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
  STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toronto
                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                       GENERAL INFORMATION:

APPLICANT: Yacoob, Reza K
APPLICANT: Yacoob, Reza K
APPLICANT: Yacoob, Reza K
APPLICANT: Zacoob, Reza K
APPLICANT: Zacoob, Reza K
APPLICANT: Zacoob, Reza K
APPLICANT: Relain, Michel H
TITLE OF INVENTION: EXPRESSION OF GENE PRODUCTS FROM
TITLE OF INVENTION: GENETICALLY MANIPULATED STRAINS OF BORDETELLA
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sin & McBurney
STREET: Other Sin & McBurney
CONTRY: Canada
ZIP: M5G IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-OSS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,526
FILING DATE: 01-DEC-1997
CLASSIFICATION: 435
ATTORNESYAGENT INFORMATION:
NAME: Steart Michael IN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09013047
Patent No. 5998168
GENERAL INFORMATION:
APPLICANT: LOOSMOINE, Sheena M.
APPLICANT: Zealey, Gavin R.
APPLICANT: Zealey, Gavin R.
APPLICANT: TILE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1038-724 MIS: jb
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330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 2.8e
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
INFORMATION FOR SEC ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                          Sequence 2, Application US/08894526
Patent No. 5942418
GENERAL INFORMATION:
45 GATFOVEVPGSOHIDSOKKAI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45 GATFQVEVPGSQHIDSQKKAI 65
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-894-526-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toronto
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                                                                                                                   US-08-894-526-2
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RESULT 14
PCT-US95-13376-21
Sequence 21, Application PC/TUS9513376
GENERAL INFORMATION:
APPLICANT: The Texas AsM University System
APPLICANT: TO Wisenbaker:
APPLICANT: College Station, Texas 77843-3369
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSCENIC PLANTS
ONRESPONDENCE: 23
CORRESPONDENCE: 23
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: TX
94.4%; Score 101; DB 4; Length 103;
95.2%; Pred. No. 2.8e-10;
Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 103;
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APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTERCOTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/00758
CURRENT APPLICAND NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101; DB 5; Length lu-
Pred. No. 2.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/328,716
FILING DATE: 24-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jones, John W. 31,380
REGISTRATION NUMBER: 36170/3P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 713-850-0165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 1, Application US/08952337
; Patent No. 6019973
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                                                                                                                  45 GATFQVEVPGSQHIDSQKKAI 65
                                                                                           1 GETFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103 amino acids
                       Best Local Similarity 95.2
Matches 20; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
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US-08-952-337-1
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  Query Match
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APPLICANT: Charles J. Arntzen, Hugh S. Mason, and Tarig A. Hag
TILLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 101; DB 4; Length 10
Pred. No. 2.8e-10;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,852
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 1301 McKinney, Suite 5100
                FILING DATE: FEBRUARY 23, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REMERENCE/DOCKET NUMBER: 1038-964
TELEPHONE: 416-595-1153
TELERAX: 416-595-1153
TELERAX: 055-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
FILING DATE: 24-OCT-1995
APPLICATION NUMBER: 08/817,906
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P01590US1
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Patent No. 6194560
  08/393,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 77010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMBUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAME: FOX, DAVIG L.
REGISTRATION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: P015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5151
TELEFAX: 713-651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFRX: 713-651-522
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 GATFQVEVPGSQHIDSQKKAI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-09-374-597-2
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
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STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-191-852-21
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94.4%; Score 101; DB 2; Length 124; ilarity 95.2%; Pred. No. 3.5e-10; Conservative 0; Mismatches 1; Indels
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APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11526.1-US-01
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FILING DATE: 24-MAY-1995
                                                                                                                                                                   APPLICATION NUMBER: US/08/747,410 FILING DATE: 12-NOV-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/694,733
FILING DATE: 02-MAX-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/271,222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREE: Amgen Inc.
STREET: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 4, Application US/08449045C; Patent No. 5770203; GENERAL INFORMATION:
   MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED VERSION 1.5.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 1152
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 GATFQVEVPGSQHIDSQKKAI 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear FORDILE TYPE: protein HYPOTHERICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: internal CS-08-747-410-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 612/332-9081
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-449-045C-4
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; Patent No. 5993820
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BAGDASARIAN, Michael
APPLICANT: IRELAND, James
; TITLE OF INVENTION: CHIMERIC LTB VACCINES
; TOWERSPONDENCE: alounce and the sequence of the
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APPLICANT: Lebens, Michael R.
TILLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1996-01-05
EARLIER APPLICATION NUMBER: ES 9501682-0
EARLIER APPLICATION NUMBER: ES 9501682-0
EARLIER FILING DATE: 1995-05-05
SOFTWARE: FASTSEQ for Windows Version 3.0
SSOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.4%; Score 101; DB 3; Length 123; llarity 95.2%; Pred. No. 3.4e-10; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 123;
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Pred. No. 3.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
EARLIER APPLICATION NUMBER: PCT/SE96/00570 EARLIER FILING DATE: 1996-05-02 EARLIER APPLICATION NUMBER: SE 9501682-0 EARLIER OF SEQ ID DATE: 1995-05-05 NUMBER OF SEQ ID NOS: 6 SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-952-337-2; Sequence 2, Application US/08952337; Patent No. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 GATFQVEVPGSQHIDSQKKAI 85
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Best Local Similarity 95.2%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Eschcerichia coli
US-08-952-337-2
                                                                                                                                                                                                                                                                                                   ; ORGANISM: Vibrio cholerae
US-08-952-337-1
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Matches 20; Conserv
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                                                                                                                                                                                               SEQ ID NO 1
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APPLICANT: Burton, Frank H.; Sutcliffe, Gregor
APPLICANT: Burton, Frank H.; Sutcliffe, Gregor
TITLE OF INVENTION: CHOLERA TOXIN GENE REGULATED BY GROWTH
HOWBORD PROWOTER
NUMBER OF SEQUENCES: 18
APPLICATION DATA:
FILING DATE: 18-MAY-1990
                                                                                                                                                                                                                                                                                               Length 124;
                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bandman, Olga
APPLICANT: Bandman, Jennifer L.
APPLICANT: CArley, Neil C.
APPLICANT: Guegler, Karl G.
APPLICANT: Gal, Preeti
APPLICANT: Gali, Surya K.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: BISEASE ASSOCIATED PROTEIN
WHERE OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                               DB 6;
4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FASISED for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,989
FILING DATE:
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                               Score 89;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF-0321 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 21
US-08-878-989-2
; Sequence 2, Application US/08878989
; Patent No. 5885803
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Billings, Lucy J J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                66 GAIFQVEVPSSQHIDSQKKAI 86
                                                                                                                                                                                                                                                                                               83.28;
85.78;
                                                                                                                                                                                                                                                                                                                                                                             1 GETFQVEVPGSQHIDSQKKAI 21
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MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                               Query Match 83.2
Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE
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5223610-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: CA
COUNTRY: U
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APPLICANT: Burnette, W. Neal
APPLICANT: Raslow, Harvey R.
APPLICANT: Kaslow, Harvey R.
TITLE OF INVENTION: RECOMBINANT DNA-DERIVED CHOLERA TOXIN
TITLE OF INVENTION: SUBUNIT ANALOGS
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Angen Inc.
STREET: 1840 De Havilland Drive
CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.2%; Score 89; DB 2; Length 124;
85.7%; Pred. No. 4e-08;
Live 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                               83.2%; Score 89; DB 1; Length 124; 85.7%; Pred. No. 4e-08;
                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/435,605A FILING DATE: 05-MAY-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/08435605A Patent No. 5874287
FILING DATE: 06-JUL-15...
ATTORNEY/AGENT IRFORMATION:
NAME: Mazza, Richard J, 657
REGIGSTRATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: A-19
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INPORMATION:
NAME: MAZZA, RICHARD J.
REGISTRATION NUMBER: 27,657
REFERENCE/DOCKET NUMBER: A-19:
INPORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                              66 GAIFQVEVPSSQHIDSQKKAI 86
                                                                                                                                                                                                                                                                                                                                                                           1 GETFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                                                                                                                                             Query Match 83.2
Best Local Similarity 85.7
Matches 18; Conservative
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                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-435-605A-12
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 19
US-08-435-605A-12
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RESULT 20

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269 GOSINVHTPNSQKVDSQKAA 288

; CLONE: 40194 US-08-878-989-2

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GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoshi
TITLE OF INVENTION: TANG-15: An Extracellular Serine Protease Overexpressed in
TITLE OF INVENTION: Breast and Ovarian Carcinomas
FILE REFERENCE: D6064
CURRENT APPLICATION NUMBER: US/09/027,337B
CURRENT FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 13
                                                                                       CYTOTACTIN DERIVATIVES THAT STIMULATE ATTACHMENT AND NEURITE OUTGROWTH, AND METHODS OF MAKING AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                Sequence 4, Application PC/TUS9511684

Sequence 4, Application PC/TUS9511684

SERERAL INFORMATION:
APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
TITLE OF INVENTION: ATTACHMENT AND NEURITE OUTGROWTH, A
TITLE OF INVENTION: AND USING SAME
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 North Torrey Pines Road, TPC 8
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/11684
FILING DATE: 14-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Logan, April C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: BEC0019P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,359
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-027-337-2; Sequence 2, Application US/09027337B; Patent No. 5972616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 1810 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 58.3°
'... 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein PCT-US95-11684-4
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                                                                                                                                                                                                                                                                     La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1. CLASSIFICATION:
                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                            COUNTRY: US
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RESULT 23
PCT-US95-11684-4
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LENGTH: 855
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                                                             Gaps
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                 50.5%; Score 54; DB 2; Length 448; 50.0%; Pred. No. 0.21;
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                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN VITLE OF INVENTION: KIRASES NUMBER OF SEQUENCES: 21 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 94304
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFEMATE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/272,796
                                                          3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF-0321 US
                                                                                                                                                                                                                                           Sequence 2, Application US/09272796
Patent No. 6207148
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Nail C.
APPLICANT: Carley, Nail C.
APPLICANT: Lal, Preeti
APPLICANT: Goli, Surya K.
APPLICANT: Goli, Surya K.
APPLICANT: Shah, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/878,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEFAX: 415-845-4166
                                                                                                                            269 GQSINVHTPNSQKVDSQKAA 288
                                                                                                  1 GETFQVEVPGSQHIDSQKKA 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.09
Matches 10; Conservative
                                     Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIEL
LIBRARY: TELL
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                   Query Match
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Pred. No. 1e+02;

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                                                                        Amino acid sequence of TADG-15 encoded by nucleotides 23\ \text{to }2589\ \text{of Sequence }1
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                                                                                                                                                                                                                                                                                                                 DB 2; Length 855; 54;
                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,364A
FILING DATE: 06-JUL-1994
CLASSIFICATION NUMBER: US 07/811,421
FILING DATE: 18-DEC-1991
PRIOR APPLICATION NUMBER: US 07/86,340
FILING DATE: 17-APR-1991
PRIOR APPLICATION NUMBER: US 07/686,340
FILING DATE: 17-APR-1991
PRIOR APPLICATION NUMBER: US 07/626,057
FILING DATE: 11-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/626,057
FILING DATE: 11-DEC-1990
PRIOR APPLICATION NUMBER: US 07/513,994
FILING DATE: 25-APR-1990
ATTONIEY/AGENT INFORMATION:
ANDER THE OFFICE OFFICE
                                                                                                                                                                                                                                                                                                                 Score 42; DB 2
Pred. No. 54;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/08271364A
| Patent No. 5756334
| GENERAL INPORMATION:
| APPLICANT: PEREEK, FRANCINE B.
| TITLE OF INVENTION: RECOMBINANT THEROMSTAB:
| CORRESPONDENCE ADDRESS:
| ADDRESSEDE: NEW ENGLAND BIOLABS, INC. STREET: 32 TOZER ROAD
| CITY: BEVERIX
| STREET: MASSACHUSETTS
| COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: WILLIAMS, GREGORY D. REGISTRANTON NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                 39.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 1022 amino acids
                                                                                                                                                                                                                                                                                                             Query Match 39.39
Best Local Similarity 50.09
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 TWNIEVPNNQHV 378
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TFQVEVPGSQHI 14
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                                                                        CTHER INFORMATION:
CTHER INFORMATION:
Patent No. 5972616
US-09-027-337-2
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US-08-271-364A-8
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38.3%; Score 41; DB 1; Length 1022;

Query Match

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Gaps
             ö
             5; Indels
             Mismatches
                                                                                                                 Search completed: July 16, 2001, 16:36:18 Job time: 207 sec
Best Local Similarity 46.7%;
Matches 7; Conservative
                                                     1 GETFQVEVPGSQHID 15
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OM protein - protein search, using sw model

July 16, 2001, 16:37:02; Search time 34.9 Seconds (without alignments) 45.836 Million cell updates/sec Run on:

US-09-786-648-5 107 Title: Perfect score: Sequence:

1 GETFOVEVPGSQHIDSQKKAI 21

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pir1:* pir2:* pir3:* PIR_68:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	heat-labile entero	cholera enterotoxi	hypothetical prote	RAD23 protein homo	hypothetical prote	hypothetical prote	kinesin heavy chai	genome polyprotein	conserved hypothet	hypothetical prote	probable carnitine	genome polyprotein	probable receptor-	ubiquitin / riboso	ubiquitin / riboso		ubiquitin (clone l	hypothetical prote	polyubiquitin 5 (c		polyubiquitin 5 (c	polyubiquitin 7 (c	tenascin precursor	probable peptide c	stress-activated p	hypothetical prote	chorismate synthas	4-aminobutyrate tr	probable peptide c
SUMMARIES	ID	QLECB	XVVCB	A86457	T04150	C96580	C86400	T49189	S15760	S78364	T19866	T49574	VFIHJH	C84726	UQDOR	UQDOR7	D34080	B27806	T04861	C34080	B34080	A27806	A34080	A32230	E82963	JC5694	S76110	S17246	JC4022	E85512
	DB	н	-	~	~	7	7	~	~	7	7	~	Н	7	-	Н	7	7	~	~	~	7	~	П	7	~	7	-	~	7
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de	Query	100.0	88.8	45.8	43.9	43.0	43.0	42.1	42.1	41.1	41.1	41.1		40.7	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	40.2	0	39.3	39.3	39.3	38.8	38.8	38.3
	Score	107	95	49	47	46	46	45	45	44	44	44	44	43.5	43	43	43	43	43	43	43	43	43	43	42	42	42	41.5	41.5	41
	Result No.	-	7	m	4	2	9	7	æ	σι	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

translation releas protein F20B17.2 [ pertussis toxin ch yaaN protein - Bac queuine tRNA-ribos hypothetical prote repressor protein inner membrane pro pyruvate carboxyla zinc finger protei DNA-directed DNA p hypothetical prote conserved hypothet conserved hypothet	<pre>mutL protein homol     translation initia     ubiquitin / riboso</pre>
E64748 C96827 A65973 A66956 T46896 T1770 C91693 G81692 A83978 A83978 T20566 T20566	S47598 H72513 UQNCR
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166 269 269 386 399 550 683 1150 1167 2911	862 148 149
	37.9 37.4 37.4
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4 4 4 4 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	44 45 45

## ALIGNMENTS

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SULT	SCB	

RESULT 1 QLECB heat-labile enterotoxin chain B precursor - Escherichia coli

C; Species: Escherichia coli C; Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change 18-Jun-1999 C; Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change 18-Jun-1999 C; Accession: A01820; B26946; I41194; I41287; I67644; A61475 R; Dallas, W.S.; Falkow, S. Nature 288, 499-501, 1980 A; Title: Anino acid sequence homology between cholera toxin and Escherichia coli heat A; Reference number: A01820; MUID:81074965

A.Accession: A01820
A.Molecule type: mRNA
A.Rocession: A01820
A.Molecule type: mRNA
A.Rocession: T. Gojobori, T.; Yokota, T.
J. Bacteriol. 169, 1352-1357, 1987
A.Title: Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichi
A.Reference number: A26946; MUID:87137303
A.Accession: B26946
A.Molecule type: DNA
A.Reference si EMBL:M5363; NID:9148335; PIDN:AAA24792.1; PID:9148336
R.Leong, J.; Vinal, A.C.; Dallas, W.S.
Infect: Immun. 48, 73-77, 1985

A;Title: Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons A;Reference number: 141194; MUID:85156481 A;Accession: 141194

A; Status: preliminary

A; Molecule type: DNA A; Residues: 1-5, 'F', 7-17, 'C', 19-24, 'S', 26-27, 'E', 29-33, 'H', 35-63, 'K', 65-66, 'A', 68-122 A; Cross-references: GB:M17874; NID:g145830; PIDN:AAA98064.1; PID:g145831 A; Experimental source: plasmid ENT-R PCG86 R; Ibrahimi, I.; Gentz, R. J. Biol. Chem. 262, 10189-10194, 1987 A; Title: A functional interaction between the signal peptide and the translation appa

ticulum.

A; Status: preliminary; translated from GB/EMBL/DDBJ A; Reference number: 141287; MUID:87280041 A; Accession: 141287

A; Molecule type: DNA A; Residues: 1-22 <RE2>

A;Cross-references: GB:M17101; NID:g146375; PIDN:AAA23973.1; PID:g146376
R;Inoue, T.; Tsuji, T.; Koto, M.; Imamura, S.; Miyama, A.
R;Inoue, T.; Tsuji, T.; Tsoli, 1993
A;Tille: Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic A;Reference number: 153542; MUID:93252225

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-17, (°, 19, 'Y', 21-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-122, 'E', 124 <R
A;Cross-references: GB:S60731; NID:9408994; PIDN:AAC60441.1; PID:9408996
B;Tsuji, T.; Lida, T.; Honda, T.; Miwatani, T.; Nagahama, M.; Sakurai, J.; Wada, K.;
Microb. Pathog. 2, 381-390, 1987

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R;Dams, E.; de Wolf, M.; Dierick, W.
Biochim. Biophys. Acta 1090, 139-141, 1991
A;Title: Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classic A;Title: Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classic A;Teference number: S17665; MUID:91355224
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-38, H', 40-67, T', 69-124 <-DA2>
A;Cross-references: EMBL:X58785; NID:948888; PIDN:CAA41591.1; PID:948890
B;Ma, O.J.: Liu, C.X.: Xiong, L.S.: Yu, X.Q.
Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. 34, 274-280, 1991
A;Title: B subunit of cholera toxin produced in Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 22-38,'H',40-67,'T',69,'E',71,'QS',74-75,'VE',78-86,'Q',88-99,'Q',101-103
A;Residues: 22-38,'H',40-67,'T',69,'E',71,'QS',74-75,'VE',78-86,'Q',88-99,'Q',101-103
B;Takao, T.; Watanabe, H.; Shimonishi, Y.
B;Takao, T.; Watenabe, H.; Shimonishi, Y.
A;Title: Facile identification of protein sequences by mass spectrometry.
A;Reference number: A21910; MUID:85126976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. Molecule type: protein
A. Residues: 22-38, "H', 40-41 < MAQ>
R. Mestalanos, "J.J.; Swartz, D.J.; Pearson, G.D.N.; Harford, N.; Groyne, F.; de Wilde, R. Meture 306, 551-57, 1983
A. Reference number: A93320; MUD:84068199
A. Accession: A05130
A. Molecule type: DNA
A. Residues: 1.32, "S', 34-74, "S', 76-124 < MEK>
A. Cross references: GB. X00171; NID:948347; PIDN:CAA24996.1; PID:9758351
A. Cross references: GB. X00171; NID:948347; PIDN:CAA24996.1; PID:9758351
A. Cross references of the beta chain of cholera enterotoxin.
A. Title: Covalent structure of the beta chain of cholera enterotoxin.
A. Fitle: Covalent structure of the beta chain of cholera enterotoxin.
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C.Complex: the cholera enterotoxin molecule contains three kinds of chains; an alpha ciate noncovalently with the subunit B, an aggregate of five beta chains
C.Function:
C.Function: involved in binding of the toxin to cell membranes
C.Superfamily: cholera enterotoxin beta chain
C.Superfamily: cholera enterotoxin toxin
F.1-21/Domain: signal sequence #status predicted <SIG>F:22-124/Product: cholera enterotoxin chain B #status predicted <MAT>
F.30-107/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 22-38,'H',40-42,'N',44-67,'T',69,'E',71-90,'N',92-124 <LAI>
A; Note: the difference at residue 70 may be due to deamidation during preparation
R; Nakashima, Y.; Napiorkowski, P.; Schafer, D.E.; Konigsberg, W.H.
FEBS Lett. 68, 275-278, 1976
A; Title: Primary structure of the B subunit of cholera enterotoxin.
A; Reference number: A38034; MUID:77026365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 252, 7249-7256, 1977

J. Biol. Cholera toxin B subunit. A;Title: Determination of the primary structure of cholera toxin B subunit. A;Reference number: A38033; MUID:78005536
A;Accession: A38033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: protein
A;Residues: 22-38,'H',40-42,'N',44-67,'T',69-90,'N',92-124 <KUR>
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A; Residues: 22-38, "H',40-42, 'N',44-67, 'T',69-90, 'N',92-124 <TAK>
A; Residues: 22-38, "H',40-42, "N',44-67, "T',69-90, "N',92-124 <TAK>
A; Experimental Source: biotype Inaba 569B
A; Note: Asn-65 was partially deaminated to Asp
C; Comment: The authors translated the codon TCA for residue 33 a
C; Genetics:
A; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 124;
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Pred. No. 4e-08;
); Mismatches
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90.5%;
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A; Accession: PC1010
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J. Biol. Ch
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    A;Title: A unique amino acid sequence of the B subunit of a heat-labile enterotoxin isol
A;Reference number: A61475, MUID:89180953
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                                                                  A Accession: AG1475
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
A; Recession: AG1475
A; Molecule type: protein
A; Recession: AG1475
A; Molecule type: protein
A; Resperimental source: strain 340-3
C; Complex: the heat-labile enterotoxin molecule contains one A chain and five or six E
C; Function:
C; Function: the biological activity of the toxin is produced by the A chain, which
C; Reywords: enterotoxin
C; Keywords: enterotoxin
F; 22-124/Product: signal sequence #status predicted <SIG>F; 22-124/Product: heat-labile enterotoxin chain B #status predicted <MAT>F; 30-107/Disulfide bonds: #status predicted
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100.0%; Pred. No. 4.6e-10;
tive 0; Mismatches 0;
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Matches 21; Conservative
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hypothetical protein AAD45990.1 [imported] - Arabidopsis thaliana Cipatyothetical protein AAD45990.1 [imported] - Arabidopsis thaliana (Gouge-ear cress) (Species: Arabidopsis thaliana (Mouse-ear cress) (Species: Arabidopsis thaliana (Mouse-ear cress) (Species: Gold (Species: Gold (Species)) (Gold (Gold (Species)) (Gold (
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C96580
C;Accession: C96580
C;Atheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, Nature 408, 816-820, 2000
A;Authors: Hunter, J.C.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: C96580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: GB: AE005173; NID: 94587538; PIDN: AAD25769.1; GSPDB: GN00141
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C; Genetics:
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NyAlternate names: protein MAA21.110
C.Species: Arabidopsis thaliana (mouse-ar cress)
C.Species: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
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Pred. No. 18;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.0%; Score 46; D
47.6%; Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA A; Residues: 1-91 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: F1511.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                  Nypothetical protein AAG21605.1 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Spacession: A86457 (Spacession: A86457 (Spacession: A86457 (Spacession: A86457 (Spacession: A86457 (Spacession: A86457 (Spain, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., Aauthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.; Koney, T.; Rowley, D.; Sakano, H. Southwick, A.M.; Sun, H.; Tallon, A.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.; Squence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gross-references: GB:AE005172; NID:g10645493; PIDN:AAG21605.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C. Accession: T04150
R. Schultz, T.F.; Quatrano, R.S.
Plant Mol. 34, 557-562, 1997
A. Title: Characterization and expression of a rice RAD23 gene.
A. Reference number: 208695; MUID:97369378
A. Sccssion: T04150
A. Sccssion: T04150
A. Status: preliminary; translated from GB/EMBL/DDBJ
A. Residues: 1-392 < SCH>
A. Residues: 1-392 < SCH>
A. Cross references: EMBL. U63530; NID:91488296; PIDN:AAB65841.1; PID:91488297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAD23 protein homolog - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr.1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A;Gene: RAD23
C;Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C96580
hypothetical protein F1511.6 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.8%; Score 49; DB
45.0%; Pred. No. 2.4;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.9%; Score 47; DB
42.9%; Pred. No. 8.1;
live 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: cv. Nipponbare
       101 ETFRVSGPGGQHRNKRDSAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 GSTFQIEVDSAQKVADVKRII 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 45.0°
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ETFOVEVPGSQHIDSQKKAI
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Best Local Similarity 42.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-255 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position: 1
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C;Accession: T49574
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
A;Accession: T49574
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, November 1996
A.Reference number: 219189
A.Reference number: 219189
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Rolecule type: DNA
A.Residues: 1-374 <WIL>
A.COSS.references: EMBL:281482; PIDN:CAB03954.2; GSPDB:GN00028; CESP:C40H5.3
A.Experimental source: clone C40H5
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T19866
R;White, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable carnitine acetyl transferase FacC [imported] - Neurospora crassa N;Alternate names: protein B208.220 C;Species: Neurospora crassa C;Species: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: X
A;Introns: 44/2; 95/1; 178/1; 234/3; 348/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C40H5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:AL355930; GSPDB:GN00116; NCSP:B208.220 A;Experimental source: BAC clone B208; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 374;
A;Genome: chloroplast
C;Superfamily: conserved hypothetical protein HI0188
C;Keywords: chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.1%; Score 44; DB 2;
42.1%; Pred. No. 57;
ive 4; Mismatches
                                                                                                                                                                                                       ;
                                                                                                                                                                                                   Score 44; DB 2
Pred. No. 16;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.1%; Score 44; DB 42.1%; Pred. No. 23; Live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              | | :|:| |:||: |:: | 30 ETVTLELPFSEHIEELKORL 49
                                                                                                                                                                                                       41.18;
40.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 GVEFHIWFPGQPHADEQKE 248
                                                                                                                                                                                                                                                                                                                                                                 2 ETFQVEVPGSQHIDSQKKAI 21
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Best Local Similarity 42.1%
".haq 8; Conservative
                                                                                                                                                                  Ouery Match
Best Local Similarity 40.07
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: NCSP:B208.220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: CESP:C40H5.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: (A; Introns: 138/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T19866
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Nichteins: RNA-directed RNA polymerase (EC 2.7.7.48)
Nicontains: RNA-directed RNA polymerase (EC 2.7.7.48)
C; Species: murine hepatitis virus, MHV
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C; Accession: S15760; S08652
R; Bredenbeek, P. U.; Pachuk, C. J.; Noten, A.F. H.; Charite, J.; Luytjes, W.; Weiss, S.R.; Nucleic Acids Res. 18, 1825-1832, 1990
A; Title: The primary structure and expression of the second open reading frame of the pc frameshifting mechanism.
A; Reference number: S15760; MUD: 90245573
A; Accession: S1576
A; Molecule type: genomic RNA
A; Residues: 1-2733 GBRE>
A; Cross-references: EMBL: X51939; NID: 958974; PID: 91334829
C; Superfamily: infectious bronchitis virus RNA-directed RNA polymerase
C; Keywords: nucleotidyltransferase; RNA biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
578364
conserved hypothetical protein 263 - Odontella sinensis chloroplast
conserved hypothetical protein 263 - Odontella sinensis
C;Species: chloroplast Odontella sinensis
C;Date: 17-Feb-1998 #sequence_revision 26-Feb-1998 #text_change 20-Jun-2000
C;Accession: 378364
R;KOwallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pancic, P.; Freier, U.
Plant Mol. Biol. Rep. 13, 336-342, 1995
A;Title: The Chloroplast Genome of a chlorophyll a+c- containing Alga, Odontella sinensi
A;Reference number: 57838
A;Accession: 578364
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-263 < KKOW>
A;Cross-references: EMBL: 267753; NID: 91185127; PIDN: CAA91737.1; PID: 91185254
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1995
C;Genetics:
A;Gene: ycf43
                                Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, submitted to the Protein Sequence Database, April 2000
A; Reference number 225018
A; Reference number 225018
A; Scheence number 225018
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-439 < RIE>
A; Cross-references: EMBL:ALL63818; GSPDB:GN00061; ATSP:MAA21.110
C; Genetics: Cultivar Columbia; BAC clone MAA21
A; Genetics: A; Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 3
A;Introns: 39/3; 74/1; 97/3; 138/3; 147/2; 193/3; 200/2; 273/3; 304/2; 341/3; 401/3
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52.9%; Pred. No. 1.3e+02;
Live 2; Mismatches 6; Indels
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Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserva
    C; Accession: T49189
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Length 864;

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C;Accession: E34000
R;Ohmachi, T.; Giorda, R.; Shaw, D.R.; Ennis, H.L.
Biochemistry 28, 5226-5231, 1989
A;Title: Molecular organization of developmentally regulated Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: E34080
A; Mocecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: GB:M23750; GB:J02858; NID:q167940; PIDN:AAA33264.1; PID:q167941
C; Superfamily: ubjquitin / Tat ribosomal protein S27a; ribosomal protein S27a homolog
C; Keywords: protein biosynthesis; protein degradation; ribosome
F;1-76/Domain: ubjquitin / #status predicted 
F;1-76/Domain: ubjquitin / #status predicted 
F;7-154/Product: ribosomal protein S27a #status predicted 
F;10-152/Domain: ribosomal protein S27a homology 
F;102-152/Domain: ribosomal protein S27a homology 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Superfamily: ubiquitin/ribosomal protein CEP52; ribosomal protein CEP52 homology; u C; Superfamily: ubiquitin protein biosynthesis; protein degradation; ribosome; zinc fi F;1-76/Product: ubiquitin #status predicted <UBI>F;1-76/Domain: ubiquitin homology <UBH>
                                                                                                                                                                                                                                                         A;Title: Complete cDNA sequence of a Dictyostelium ubiquitin with a carboxy-terminal A;Reference number: S00357; MUID:88152253 A;Accession: S00357
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                                                                               NiAlternate names: ubiquitin fusion protein
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Bate: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
C;Accession: S00357; A2586
C;Accession: S0357; A2586
FEBS Lett. 229, 273-278, 1988
                                                            ubiquitin / ribosomal protein CEP52 - slime mold (Dictyostellum discoideum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Dictyostelium discoideum
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jul-2000
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C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 23-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ribosomal protein S27a - slime mold (Dictyostelium discoideum)
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                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-128 <MUE>
A; Cross-references: EMBL:X07210; NID:g7381; PIDN:CAA30183.1; PID:g7382
A; Experimental source: strain AX2-214
C; Genetics:
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F;77-128/Domain: ribosomal protein CEP52 homology <CPH>
F;95-114/Region: zinc finger CCCC motif
F;121-128/Region: nuclear location signal
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13;
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Mismatches
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Pred. No. 1
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Pred. No.
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Best Local Similarity 42.2
Local 9, Conservative
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Best Local Similarity
Matches 9; Conserv
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84726
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A;Tille, Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: C84726
A;Accession: C84726
A;Accession: C84726
A;Accession: C84726
A;Cross-references: GB:AE002093; NID:94887748; PIDN:AAD32284.1; GSPDB:GN00139
C;Genetics: A;Aap31880
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                   A Accession: B36815
A.Molecule type: genomic RNA
A.Molecule type: genomic RNA
A.Residues: 1-2731 <a href="Libbo">Libba</a>
A.Cross-references: GB:M55148; NID:g331851; PIDN:AAA46458.1; PID:g331853
A.Cross-references: GB:M55148; NID:g331851; PIDN:AAA46458.1; PID:g331853
R.Lee, H.J.; Shah, C.K.; Gorbalenya, A.E.; Koonin, E.V.; La Monica, N.; Tuler, J.; Bag6
Virology 180, 567-582, 1991
A.Title: The complete sequence (22 kilobases) of murine coronavirus gene 1 encoding the
A.Reference number: A38547; MUID:91111976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3
                                                                                                                                                                                                                                                                           C; Accession: B36815
R; Lee, H.J.; Shieh, C.K.; Gorbalenya, A.E.; Koonin, E.V.; La Monica, N.; Tuler, J.; Bagó subultted to Genbank, February 1991
A; Description: The complete sequence (22 kilobases) of murine coronavirus gene 1 encodin A; Reference number: A36815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Contents: annotation
A.Note: neither nuclectide nor complete amino acid sequence is given
C.Comment: This protein may be translated as a la-1b polyprotein by a ribosomal frameshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: infectious bronchitis virus RNA-directed RNA polymerase
C;Keywords: glycoprotein; nucleotidyltransferase; RNA blosynthesis
F;269,304,785,1184,1287,1524,1842,2196,2575,2630,2645,2665/Binding site: carbohydrate
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                                                                                                                                                                 N,Alternate names: 1b protein
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: murine hepatitis virus, MHV
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 11-Jun-1999
C;Accession: B36815
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Pred. No. 50;
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50.0%;
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   QTFWADAPGDAKIDALRKA
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Best Local Similarity
Matches 11; Conserv
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C. Accession: B34080
R; Ohmachi, T.; Giorda, R.; Shaw, D.R.; Ennis, H.L.
Biochemistry 28, 525-5231, 1989
A; Title: Molecular organization of developmentally regulated Dictyostellum discoideum A; Reference number: A34080; MUID:89352609
A; Accession: B34080
A; Reference number: A34080; MUID:89352609
A; Reference number: A34080; MUID:89352609
A; Status: pretliminary
A; Residues: 1380 COHM>
A; Residues: 1380 COHM>
A; Cross-references: GB:M23748
A; Cross-references: GB:M23748
C; Superimental source: strain B, clone DCUB19
C; Superimental; polyubiquitin 5; ubiquitin homology
C; Keywords: nucleus; polyprotein; protein degradation
F; 1-76/Domain: ubiquitin homology < UBH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Ohmachi, T.; Glorda, R.; Shaw, D.R.; Ennis, H.L.
Biochemistry 28, 5226-5231, 1989
A;Title: Molecular organization of developmentally regulated Dictyostellum discoldeum A;Reference number: A34080; MUID:89352609
A;Steference number: A34080
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                             N;Alternate names: ubiquitin 2
C;Species: Dictyostelium discoideum
C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 11-Apr-1997
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C.Species: Dictyostelium discoideum
C.Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 11-Apr-1997
                                                                                                                                                           Gaps
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    slime mold (Dictyostelium discoideum)

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                                                                                               Length 368;
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A; Cross-references: GB:M23754
A; Experimental source: strain B, clone DCUB12
C; Superfamily: polyubiquitin 5; ubiquitin homology
C; Keywords: nucleus; polyprotein; protein degradation
F;1-76/Product: ubiquitin #status predicted CUB1>
F;1-76/Domain: ubiquitin homology CUB1>
F;77-152/Product: ubiquitin #status predicted CUB2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;77-152/Domain: ubiquitin homology <UBH2>
F;153-228/Product: ubiquitin #status predicted <UB3>
F;153-228/Domain: ubiquitin homology <UBH3>
F;229-304/Product: ubiquitin #status predicted <UB4>
F;229-304/Promain: ubiquitin #status predicted <UB4>
F;325-304/Domain: ubiquitin homology <UB4>
F;305-380/Domain: ubiquitin #status predicted <UB5>
F;305-380/Domain: ubiquitin homology <UB5>
F;305-380/Domain: ubiquitin homology <UB5>
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                                                                                                                                                           Mismatches
                                                                                                  Score 43;
Pred. No.
                                                                                                                                                     7;
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                                                                                                  40.2%;
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ilarity 42.9%;
Conservative
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Best Local Similarity
Matches 6; Conserva
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Best Local Similarity
Matches 9; Conserv
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                 A; Note: F28A21.100
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B27806
ubiquitin (clone lambda229) - slime mold (Dictyostellum discoideum)
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Species: Dictyostellum discoideum
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 06-Feb-1998
C;Accession: B27806
R;Glooda, R:Ennis, H.L.
Mol. Cell. Biol. 7, 2097-2103, 1987
A;Title: Structure of two developmentally regulated Dictyostellum discoideum ubiquitin gA;Reference number: A27806; MUID:87257921
A;Reference number: A27806; MUID:87257921
A;Residues: 1-229 cGIO>
A;Cross-references: GB:M23754
C;Superfamily: polyubiquitin 3; ubiquitin homology
C;Seywords: duplication; nucleus; polyprotein; protein degradation
F;1-76/Domain: ubiquitin homology cUBHI>
F;77-152/Domain: ubiquitin homology cUBH3>
F;153-228/Domain: ubiquitin homology cUBH3>
C: Accession: D34080
R: Obmachi, T.: Glorda, R.; Shaw, D.R.; Ennis, H.L.
B: Obmachi, T.: Glorda, R.; Shaw, D.R.; Ennis, H.L.
B: December 1 2 226-5231, 1989
A: Title: Molecular organization of developmentally regulated Dictyostelium discoideum ub
A: Reference number: A34080; MUID: 89352609
A: Accession: D34080
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-28 COHM>
A: Residues: 1-28 COHM>
A: Coss-references: GB:M23751
C; Superfamily: polyubiquitin 3; ubiquitin homology
C; Keywords: duplication; nucleus; polyprotein; protein degradation
C; Keywords: duplication; nucleus; polyprotein; protein degradation
F: 1-76/Domain: ubiquitin homology <UBH1>
F: 153-228/Domain: ubiquitin homology <UBH3>
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C;Accession: T04861
R;Bevan, M.; Mueller, M.W.; Muendlein, A.; Felber, R.; Bancroft, I.; Mewes, H.W.; Mayer, Bubmitted to the Protein Sequence Database, February 1999
A;Reference number: Z15387
A;Accession: T04861
A;Molecule type: DNA
A;Residues: 1-368 cBEV>
A;Cross-references: EMBL:AL035526
A;Cross-references: EMBL:AL035526
A;Experimental source: cultivar Columbia; BAC clone F28A21
C;Genetics:
A;Map position: 4
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ed. No. 20;
Mismatches
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42.9%; Pred. No. 20;
Live 5; Mismatches
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Pred. No.
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Best Local Similarity 42.9*
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Best Local Similarity 42.9
Matches 9; Conservative
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polyubiquitin 7; ubiquitin homology
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Best Local Similarity 42.9
Matches 9; Conservative
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C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 30-Mar-1990 #sequence_revision 30-Mar-1990 #text_change 11-Apr-1997
C;Accession: A34080
R;Ohmachi, T.; Giorda, R.; Shaw, D.R.; Ennis, H.L.
Biochemistry 28, 5226-5231, 1989
A;Title: Molecular organization of developmentally regulated Dictyostelium discoideum ub
A;Reference number: A34080; MUID:89352609
A;Status: preliminary
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R;Glorda, R.; Ennis, H.L.
Mol. Cell. Biol. 7, 2097-2103, 1987
A;Title: Structure of two developmentally regulated Dictyostellum discoideum ubiquitin A;Reference number: A27806; MUD:87257921
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A; Residues: 1-381 <GIO>
A; Colore type: mRNA
A; Residues: 1-381 <GIO>
A; Cross references: EMBL: MI9491; NID:g167950; PIDN:AAA33269.1; PID:g167951
A; Experimental source: strain B, clone pik229
C; Superfamily: polyubiquitin 5; ubiquitin homology
C; Superfamily: polyubiquitin 5; ubiquitin homology
C; Reywords: nucleus; polyprotein; protein degradation
F; 1-76/Pomain: ubiquitin #status predicted <UB1>
F; 1-76/Pomain: ubiquitin homology <UBH2>
F; 153-228/Pomain: ubiquitin #status predicted <UB3>
F; 153-228/Pomain: ubiquitin homology <UBH3>
F; 153-34/Pomain: ubiquitin homology <UBH3>
F; 229-304/Pomain: ubiquitin homology <UBH4>
F; 305-380/Pomain: ubiquitin #status predicted <UB5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polyubiquitin 5 (clone pLK229) - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 23-Jul-1999
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                                                                                                                                                                                                                                                                                                                     ore 43; DB 2; Length 380;
ed. No. 35;
Mismatches 7; Indels
                                                         F)153-228/Product: ubiquitin #status predicted <uB3>
F)153-228/Domain: ubiquitin homology <uBH3>
F)229-304/Product: ubiquitin #status predicted <uB4>
F)229-304/Domain: ubiquitin homology <uBH4>
F)305-380/Droduct: ubiquitin #status predicted <uB5>
F)305-380/Domain: ubiquitin homology <uB1>
F;77-152/Product: ubiquitin #status predicted <UB2>
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A;Residues: 1-532 <OHM>
A;Cross-refrances: GB:M3753
A;Experimental source: strain B, clone DCUB14
                                                                                                                                                                                                                                                                                                                     Query Match 40.2%; Score 43; Best Local Similarity 42.9%; Pred. No. Matches 9; Conservative 5; Mismatch
                              77-152/Domain: ubiquitin homology
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Best Local Similarity
Matches 9; Conserv
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N'Alternate names: cytotactin; hexabrachion
N'Contains: tenascin 190K; tenascin 200K
C; Species: Gallus gallus (chicken)
C; Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: A32230; B32230; A33379; B33379; C33379; S01292; A30903
R; Jones, F. S.; Hoffman, S.; Cunningham, B. A.; Edelman, G.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1905-1909, 1989
A; Title: A detailed structural model of cytotactin: protein homologies, alternative R
A; Reference number: A32230; MUID:89184536
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Cross-references: GB:J04519
B; Spring, J; Beck, K; Chiquet-Ehrismann, R.
Cell 59, 325-334, 1989
A; Title: fwo contrary functions of tenascin: dissection of the active sites by recomb
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A;Cross-references: GB:M23121
R;Pearson, C.A.; Pearson, D.; Shibahara, S.; Hofsteenge, J.; Chiquet-Ehrismann, R.
EMBO J. 7, 2977-2982, 1988
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A; Residues: 1-204, 'G', 206-221, 'A', 223-380, 'D', 382-386, 'H', 388-444, 'HN', 447-450, 'V', 45
A; Residues: 1-204, 'G', 206-221, 'A', 223-380, 'D', 382-386, 'H', 388-444, 'HN', 447-450, 'V', 45
A; Rccession: B33379
A; Accession: B33379
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A:Accession: C33379
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A;Residues: 1-1810 <JON>
A;Cross-references: GB:J04519; NID:g211717; PIDN:AAA48745.1; PID:g211718
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                                                                                                               Fig. 7-152/Product: ubiquitin #status predicted <UB2>
Fig. 7-152/Domain: ubiquitin #status predicted <UB2>
Fig. 7-152/Domain: ubiquitin #status predicted <UB3>
Fig. 7-28/Product: ubiquitin homology <UBH3>
Fig. 229-304/Product: ubiquitin homology <UBH3>
Fig. 239-304/Product: ubiquitin #status predicted <UB4>
Fig. 239-304/Domain: ubiquitin #status predicted <UB4>
Fig. 380-780/Product: ubiquitin homology <UBH5>
Fig. 381-456/Product: ubiquitin homology <UBH5>
Fig. 381-456/Product: ubiquitin #status predicted <UB6>
Fig. 381-456/Domain: ubiquitin homology <UBH6>
Fig. 532/Product: ubiquitin homology <UBH6>
Fig. 7-332/Product: ubiquitin homology <UBH6>
Fig. 7-532/Product: ubiquitin homology <UBH7>
Fig. 7-532/Domain: ubiquitin homology <UBH7>
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C; Keywords: nucleus; polyprotein; protein degradation F;1-76/Product: ubiquitin #status predicted <UBl>
F;1-76/Domain: ubiquitin homology <UBH1>
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A; Accession: A33379
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Length 427; 5; Indels

2; DB 7

0; Mismatches Score 42; Pred. No.

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A; Status: nucleic acid sequence not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-427 < HAS>
A; Residues: 1-427 < HAS>
A; Cross-references: DDBJ: AB001744; NID: 92467307; PIDN: BAA22598.1; PID: 41023466; PID: 9
C; Comment: This enzyme is a mitogen-activated protein kinase, and plays a role in egg
C; Comment: unassigned Ser. Thr or Tyr-specific protein kinases; protein kinase hom C; Keywords: phosphotransferase
F; 24-278/Domain: protein kinase homology < KIN>
                                                                          A;Title: Structure and expression of carp mitogen-activated protein kinases homologou A;Reference number: JC5693; MUID:97456373
                R;Hashimoto, H.; Matsuo, Y.; Yokoyama, Y.; Toyohara, H.; Sakaguchi, J. Biochem. 122, 381-386, 1997
A;Title: Structure and expression of carp mitogen-activated protein
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61.5%;
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Best Local Similarity 61.5
Matches 8; Conservative
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A; Molecule type: mRNA
A; Residues: 27-181, 'R',183-204,'G',206-221,'A',223-380,'D',382-386,'H',388-444,'HN',447-A; Cross-references: ExBL:X0030
A; Orote: part of this sequence was confirmed by protein sequencing
C; Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type
C; Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin
F;1-22/Domain: signal sequence #status predicted <SIG>F;23-33/Domain: signal sequence #status predicted <AMT>
F;23-33/Domain: propeptide #status predicted <AMT>
F;23-249/Domain: propeptide #status predicted <AMT>
F;23-249/Domain: EGF homology <EGF>
F;34-1810/Product: tenascin 230K #status predicted <AMT>
F;23-249/Domain: EGF homology <EGF>
F;34-1810/Product: tenascin type III repeat homology <FN3D>
F;36-73/Domain: fibronectin type III repeat homology <FN3D>
F;36-73/Domain: fibronectin type III repeat homology <FN3D>
F;36-349/Domain: fibronectin type III repeat homology <FN3D>
F;316-340/Domain: fibronectin type III repeat homology <FN3D>
F;318-139/Domain: fibronectin type III repeat homology <FN3D>
F;3407-1487/Domain: fibronectin type III repeat homology <FN3D>
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E82063
probable peptide chain release factor PA5470 [imported] - Pseudomonas aeruginosa (strain c; Species: Pseudomonas aeruginosa
C; Species: Pseudomonas aeruginosa
C; Date: 15-Sep-2000
C; Accession: BE2963
R; Stcover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Vuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A.71tle: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathon A; Reference number: A82950; MUID: 20437337
A; Accession: B82963
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-204 <STO>A; Cross-references: GB:AE004959; GB:AE004091; NID: 99951791; PIDN:AAG08855.1; GSPDB:GN001
A; Experimental source: strain PA01
C; Genetics:
A; Gene: PA5470
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C; Species: 20-Nov-1997 #sequence_revision 20-Nov-1997 #text_change 24-Sep-1999 C; Accession: JC5694
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Pred. No. 1.8e+02;
2; Mismatches 3; Indels
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STRAIN=ISOLATE P307;
MEDLINE=ISOLATE P307;
Dallas W.S., Falkow S.,
"Amino acid sequence homology between cholera toxin and Escherichia coli heat-labile toxin.";
Nature 288:499-501(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=ISOLATE P307;
MEDLINE=85156481; PubWed=3884513;
Leong J., Vinal A.C., Dallas W.S.;
"Nucleotide sequence comparison between heat-labile toxin B-subunit c1strons from Escherichia coli of human and porcine origin.";
Infect. Immun. 48:73-77(1985).
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STRAIN-ISOLATE PCG86;
MEDLINE-87137303; bubmed-3546273;
Yamamoto T., Gojobori T., Yokota T.;
"Evolutionary origin of pathogenic determinants in enterotoxigenic Escherichia coli and Vibrio cholerae Ol.";
                                                                                                                                                                                                     P32890; P13768; P01557; 21-301-1986 (Rel. 01, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HEAT-LABILE ENTEROTOXIN B CHAIN PRECURSOR (LT-B; PORCINE) (LTP-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sixma T.K., van Zanten B.A.M., Dauter Z., Hol W.G.J.;
"Refined structure of Escherichia coli heat-labile enterotoxin, a close relative of cholera toxin.";
J. Mol. Biol. 230:890-918(1993).
[6]
X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-91238966; PubMed=2034287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-22 FROM N.A.

MEDIAND=87280041; PubMed=3301830;
Ibrahimi I., Gentz R.,

"A functional interaction between the signal peptide and the translation apparatus is detected by the use of a single point mutation which blocks translocation across mammalian endoplasmic reticulum.";
                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
P75049 075570 09540
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028589
050313
P27420
P53699
P14882
P36598
                                                                                                                                                   ALIGNMENTS
                    SR54_THEAC
IL7R_MOUSE
CD5_RAT
INR1_SHEEP
BCHD_CHLVI
HS7C_CAEEL
CC4_CANAL
                                                                                                      THI1_SCHPO
DPOL_HPBVM
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MEDLINE-93240541; PubMed-8478941;
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                                                                                               PCCA_RAT
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REVISIONS TO 28 AND 64.
Escherichia coli
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Copyright (c) 1993 - 2000 Comp
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124 AA

PRT;

STANDARD;

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MEDLINE-93252225; PubMed-8486242;
Inoue T., Tsuji T., Koto M., Imamura S., Miyama A.;
"Amino acid sequence of heat-labile enterotoxin from chicken
"Amino acid sequence of heat-labile enterotoxin from chicken
enterotoxigenic Escherichia coli is identical to that of human strain
                                                                                                                                                                                                                                                                                                                MEDLINE-83114628; PubMed-6759877;
Yamamoto T., Tamura T.A., Yokota T., Takano T.;
"Overlapping genes in the hear-labile enterotoxin operon originating from Escherichia coli human strain.";
Mol. Gen. Genet. 188:356-359(1982).
                                                                                                                                                                                                                      Leong J., Vinal A.C., Dallas W.S.; "Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons from Escherichia coli of human and porcine origin."; Infect. Immun. 48:73-77(1985).
                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HEAT-LABILE ENTEROTOXIN B CHAIN PRECURSOR (LT-B, HUMAN) (LTH-B).
                                                                                                                    Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R
"Identification of errors among database sequence entries and
comparison of correct amino acid sequences for the heat-labile
enterotoxins. of Escherichia coli and Vibrio cholerae.";
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Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEMS Microbiol. Lett. 108:157-161(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (3.04 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Microbiol. 15:1165-1167(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISCUSSION OF SEQUENCE. MEDLINE-95349400; PubMed-7623669;
                                                                                                                                                                                                 STRAIN=ISOLATE H74-114;
MEDLINE-85156481; PubMed-3884513;
                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-ISOLATE H74-114;
                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-ISOLATE H10407;
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-ISOLATE H10407;
                                                   01-JAN-1990 (Rel. 13,
01-JAN-1990 (Rel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-ETEC LT 87;
                                                                                                                                                           NCBI_TaxID=562;
                                                                                                         ELTB OR LTPB.
                                                                                                                                               Escherichia
                            ELBH_ECOLI
                                        P1381
             ELBH_ECOLI
                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@189-sib.ch).
Sixma T.K., Pronk S.E., Kalk K.H., Wartna E.S., van Zanten B.A.M., Witholt B., Hol W.G.J.; "Crystal structure of a cholera toxin-related heat-labile enterotoxin
                                                                                       MEDLINE-95349400: PubMed-7623669;

Domenighini M., Pizza M., Jobling .M.G., Holmes R.K., Rappuoli R.;

Identification of errors among database sequence entries and
comparison of correct amino acid sequences for the heat-labile
enterotoxins of Escherichia coli and Vibrio cholerae.",
Mol. Microbiol. 15:1165-1167(1995).

-I- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED BY
THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-I- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterotoxin; Signal; 3D-structure.
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                                                                                                                                                                                                                                                                                                                               EMBL; M17873; AAA98065.1; -.
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                                                     Nature 351:371-377(1991).
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1HTL; 20-APR-95.
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1LTB; 31-JAN-94
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1LT5; 03-DEC-97
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B26946; QLECER
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the European Bioinformatics Institute. There are no restrictions on
use by non-profit institutions as long as its content is in no
enterotoxin carrying peptides with anti-herpes simplex virus type
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                                                                                                                                                                                                               J. Biol. Chem. 274:8764-8769(1999).
-!- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.
-!- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE
                                                                                                                                                                            activity,";
T. Biol, Chem. 274:8764-8769(1999)
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100.0%; Score 107; DB 1; 100.0%; Pred. No. 3.2e-10; Mismatches

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Conservative

Best Local Similarity Matches 21; Conserv

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Query Match

GETFQVEVPGSQHIDSQKKAI 86 GETFQVEVPGSQHIDSQKKAI 21

Length 124; Indels

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PIR; A01819; XVVCB
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STRAIN-EL TOR 2125;
MEDLINE-84068199; PubMed-6646234;
Mekalanos J.J., Swartz D.J., Pearson G.D.N., Harford N., Groyne F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yamamoto K., Do V.G.R.F., Xu M., Iida T., Miwatani T., Albert M.J.,
Honda T.;
                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                          Lockman H., Kaper J.B.; "Nucleotide sequence analysis of the A2 and B subunits of Vibrio cholerae enterotoxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Cholera toxin genes: nucleotide sequence, deletion analysis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lebens M., Holmgren J., "Structure and arrangement of the cholera toxin genes in Vibrio
                                                                                                                                                                                ;
                                                                                    HEAT-LABILE ENTEROTOXIN B CHAIN.
                                                                                                                                                            Query Match 94.4%; Score 101; DB 1; Length 124; Best Local Similarity 95.2%; Pred. No. 2.9e-09; Matches 20; Conservative 0; Mismatches 1; Indels
                                                                                                               H10407).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=EL TOR 2125;
Dams E., de Wolf M., Dierick W.;
Submitted (MAY-1991) to the EMBL/GenBank/DDBJ databases.
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H -> Y (IN ISOLATE H
H -> R (IN ISOLATE H
V; E9F7F7C7B9D3BC47 C
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13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-2000 (Rel. 05, Last sequence update)
CHOLCT-2000 (Rel. 40, Last annotation update)
CHOLERA ENTEROTOXIN, BETA CHAIN PRECURSOR.
CIXB OR TOXB OR VC1456.
                                                                                                                                                                                                                                                                    124 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cholerae 0139.";
FEMS Microbiol. Lett. 117:197-202(1994).
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                                                                                                                                                                                                                                                                    PRT;
                                                                 Enterotoxin; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=84061784; PubMed=6315707;
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MEDLINE-94237453; PubMed-8181723;
                                              Pfam; PF01376; Enterotoxin B; 1. PRINTS; PR00772; ENTEROTOXINB.
                                                                                                              20 H
34 H
14027 MW;
                                                                                                                                                                                                   1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                            66 GATFQVEVPGSQHIDSQKKAI 86
EMBL; J01646; AAB02982.1; -. EMBL; S60731; AAC60441.1; -. EMBL; X83966; CAAS8800.1; -. PDB; LLTR; 23-MAR-99.
InterPro; IPR001835; -.
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STRAIN*1854 / O139-BENGAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine development.";
Nature 306:551-557(1983).
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AEDLINE-EL TOR NIG961 / SEROTYPE 01;
MEDLINE-20406833; PubMed=10952301;
Heldeblerg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Raed T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
MEDLINE=95387394; PubMed=7658472;
Zhang Yu. Westbrook M.L., Westbrook M.L., Otwinowski Z.,
Maulik P.R., Reed R.A., Shipley G.G.;
"The 2.4 A crystal structure of cholera toxin B subunit pentamer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING TO CELL MEMBRANES.
--- SUBDINIT: CONTAINS 3 KINDS OF CHAINS. AN ALPHA AND A GAMMA CHAIN (FROW THE SAME PRECURES MOLECULE), LINKED BY AN INTERCHAIN DISULFIDE BOND, ASSOCIATE NONCOVALENTLY WITH AN AGGREGATE OF 4 TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Determination of the primary structure of cholera toxin B subunit."; J. Biol. Chem. 252:7249-7256(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Merritt E.A., Sarfaty S., van den Akker F., L'Hoir C., Martial J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Crystal structure of cholera toxin B-pentamer bound to receptor GM1
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STRAIN-OGRAMA 41 / CLASSICAL BIONYPE;
MEDLINE-97376625; PubMed-9232653;
MERLITE E.A., Sarfaty S., Jobling M.G., Chang T., Holmes R.K.,
Hirst T.R., Hol W.G.J.;
"Structural studies of receptor binding by cholera toxin mutants.";
"Structural studies of receptor binding by cholera toxin mutants.";
"Structural Sci. 6.1516-1528 (1997).
-1- FUNCTION: THE BETA CHAIN AGGREGATE (B SUBUNIT) IS INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                        'DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-78005537; Pubmed-903363;
Kurosky A., Markel D.E., Peterson J.W.;
"Covalent structure of the beta chain of cholera enterotoxin.";
J. Biol. Chem. 252:7257-7264(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE-94272319; Pubmed-8003954;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein Sci. 3:166-175(1994).
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EMBL; X76391; CAA53976.1; --
EMBL; AE004224; AAF94613.1;
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EMBL; 267753; CAA91737.1; -. Mendel; 5328; ODOsi; ycf43;1. InterPro; IPR002033; -.
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-90245573; PubMed-2159623; Bredenbeek P.J., Pachuk C.J., Noten A.F.H., Charite J., Luytjes W., Weiss S.R., Span W.J.M.; Write primary structure and expression of the second open reading frame of the polymerase gene of the coronairus MHV-A59; a highly conserved polymerase is expressed by an efficient ribosomal frameshifting mechanism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine coronavirus MHV (strain A59).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                     CHOLERA ENTEROTOXIN, BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 88.8%; Score 95; DB 1; Length 124; Best Local Similarity 90.5%; Pred. No. 2.6e-08; Matches 19; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                        | REF. 7 AND 8).
| REF. 8).
| REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9AA393E3EA8E3EBF CRC64;
                                                                                                                                                                                                                                                                              AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (ORF1B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2733 AA.
                                                                                                                                                                                                      Membrane; Enterotoxin; Signal; 3D-structure.
                                                                                                                                                                                                                                                                  ^ ^ ^ ^ ^ ^ ^ ^ ^
                                                                                                                                                        InterPro; IPR001835; -. Pfam; PF01376; Enterotoxin_B; 1. PRINTS; PR00772; ENTEROTOXINB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13957 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 GAIFQVEVPGSQHIDSQKKAI 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                      03-DEC-97.
12-AUG-98.
08-MAR-96.
08-MAR-96.
23-DEC-96.
01-AUG-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=11142;
                                                                                                                                            VC1456;
            S14624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RRPB_CVMA5
ID RRPB_CVMA5
AC P16342;
DT 01-AUG-1990
                                                                       1CHO;
                                                                                                                  1XTC;
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SEQUENCE
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PIR;
PIR;
PDB;
PDB;
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PDB;
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Nucleic Acids Res. 18:1825-1832(1990).

-!- FUNCTION: THE RNA DEPRNDENT RNA POLYMERASE OF CORONAVIRUSES IS

A MULTIFUNCTIONAL PROTEIN: IT CONTAINS THE ACTIVITIES NECESSARY
FOR THE TRANSCRIPTION OF NEGATIVE STRANDED RNA, LEADER RNA,
SUBGENOMIC MRNAS AND PROGENY VIRION RNA.

-!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

Kowallik K.V., Stoebe B., Schaffran I., Kroth-Pancic P., Freier U.;

"The chloroplast genome of a chlorophyll a+c-containing alga,
Odontella sinensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; XJLSS; CLESS; S08652.
PIR; S18760; S15760.
PIR; S15760; S15760.
Transferase; RNA-directed RNA polymerase; Helicase; ATP-binding.
POLYMERASE.
POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Odontella sinensis."; ... Plant Mol. Biol. Rep. 13:336-342(1995).
-! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE TATC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; stramenopiles; Bacillariophyta; Coscinodiscophyceae;
Biddulphiophycidae; Eupodiscales; Eupodiscaceae; Odontella.
NCBI_TaxID=2839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                       -!- MISCELLANEOUS: THIS PROTEIN MAY BE TRANSLATED AS A 1A-1B POLYPROTEIN BY A RIBOSOMAL FRAMESHIFTING MECHANISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 45; DB 1; Length 2733;
Pred. No. 66;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 CYS/HIS-RICH.
06 HELICASE.
27 ATP (BY SIMILARITY).
309218 MW; F3ACCREF20D20C41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
PROTEIN YCF43 (ORF263).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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01-FEB-1996 (Rel. 33, Last seq
01-CCT-2000 (Rel. 40, Last ann
HYPOTHETICAL 30.1 KDA PROTEIN
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52.9%;
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Transferase;
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01-AUG-1988
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UBIQUITIN.
                                             RRPB_CVMJH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UBIQ_DICDI
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                         RESULT 7
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UBIQ_DICDI
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                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                    Grossman A., Mittrucker H.W., Antonio L., Ozato K., Mak T.W.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 1; Length 467;
Pred. No. 14;
6; Mismatches 4; Indels
                                                                                                                                       Length 263;
                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Grafham D.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE IRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transcription regulation; DNA-binding; Nuclear protein. DNA_BIND 9 111 TRYPTOPHAN PENTAD REPEAT.
                                                                                                        30080 MW; . 25083364F2A89E88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7E28F5E0F5BA4053 CRC64;
                           Transmembrane
                                                                                                                                       1;
                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updatu
INTERFERON REGULATORY FACTOR 6 (IRF-6).
                                                                                                                                      Score 44; DB Pred. No. 7.8;
                                                                                                                                                         Mismatches
                                           POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                        Chloroplast; Hypothetical protein; Tran
TRANSMEM 53 73 POTENTIAL.
                                                                                                POTENTIAL
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9
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15-JUL-1998 (Rel. 36, Last seq
15-JUL-1999 (Rel. 38, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF027292; AAB84111.1; -. EMBL; AL022398; CAA18545.1; -. HSSP; P23906; 11RG.
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PROSITE; PS00601; IRF; 1.
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                                                                                                                                    41.18;
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                                                                                                                                                                                         41.18;
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273 QVKFPGPEHITNEKQKL 289
Pfam; PF00902; UPF0032; 1.
                                                                                                                                                                             2 ETFOVEVPGSOHIDSOKKAI
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                                                                                                                                                          Conservative
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Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                   STANDARD;
                PROSITE; PS01218; TATC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001346; -.
                                            123
150
173
                                                                         201
                                                                                                                           Ouery Match
Best Local Similarity
'-has 8; Conserv?
                                                                                                                                                                                                                                                                                                                         (Human)
                                                                                    213
241
263 AA;
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                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                   IRF6_HUMAN
014896;
                                           TRANSMEM
TRANSMEM
TRANSMEM
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TRANSMEM
SEQUENCE
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A MULTIFUNCTIONAL PROTEIN: IT CONTAINS THE ACTIVITIES NECESSARY
FOR THE TRANSCRIPTION OF NEGATIVE STRANDED RNA, LEADER RNA,
SUBGENOMIC MRNAS AND PROGENY VIRION RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDIATE-9111975; PubMed-1846489; MEDIATE-9111975; PubMed-1846489; Lee H.-J., Shieh C.-K., Gorbalenya A.E., Koonin E.V., la Monica N., Tuler J., Bagdzhardzhyan A., Lai M.M.C.; Tuler J., Lai M.M.C.; Tuler J., Shill J., Lai M. M.C.; Tuler J., Lai M. M.C.; Lai M.
                                                                                                                                                                                                                                                                                                Murine coronavirus MHV (strain JHM).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA-directed RNA polymerase; Helicase; ATP-binding.
522 824 POLYMERASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 2731;
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73B3C4025244CEE5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
                                                                                            01-APR-1993 (Rel. 25, Created)
1-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RNA-DIRECTED RNA POLYMERASE (EC 2.7.7.48) (ORF1B).
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2731 AA
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HELICASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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Pred. No.
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MEDLINE-88152253; PubMed=2831095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308834 MW;
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69.28;
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hes 9; Conservative
STANDARD;
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SEQUENCE
              BINDING
                           VARIANT
                                                                                                                                                                                                                                                                                                                       Gallus
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TENA_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                      "Complete cDNA sequence of a Dictyostelium ubiquitin with a carboxy-terminal tail and identification of the protein using an anti-peptide
                                                                                                                                                                                                                                                                                         Westphal M., Mueller-Taubenberg A., Noegel A., Gerisch G.;
"Transcript regulation and carboxyterminal extension of ubiquitin in Dictyostelium discoleum.";
FEBS Lett. 209:92-96(1986).
-!- FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
                                                                                                                                                                                       MEDLINE-87257921; PubMed-3037345; Giorda R., Ennis H.L.; "Structure of two developmentally regulated Dictyostellum discoideum ubiquitin genes."; MOI. Cell. Biol. 7:2097-2103(1987).
                                                                                                                                                                                                                                                                                                                                                                                                        MISCELLANEOUS: UBIQUITIN IS SYMTHESIZED AS A POLYUBIQUITIN PRECURSOR WITH EXACT HEAD TO TAIL REPEATS. SOME UBIQUITIN GENES CONTAIN A SINGLE COPY OF UBIQUITIN FUSED TO A RIBOSOMAL PROTEIN.
                                                                                                           Ohmachi T., Giorda R., Shaw D.R., Ennis H.L.; "Molecular organization of developmentally regulated Dictyostelium discoideum ubiquitin cDNAs."; Biochemistry 28:5226-5231(1989).
 Mueller-Taubenberger A., Westphal M., Jaeger E., Noegel A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NECESSARY FOR BRANCHED-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X07210; CAA30183.1; ALT_TERM. EMBL; M19666; AAA33261.1; ALT_TERM. EMBL; M19492; AAA33261.1; ALT_TERM. EMBL; M23748; AAA33263.1; ALT_TERM. EMBL; M23749; AAA33263.1; ALT_TERM. EMBL; M23750; AAA33263.1; ALT_TERM. EMBL; M23751; AAA33265.1; ALT_TERM. EMBL; M23751; AAA33266.1; ALT_TERM. EMBL; M23754; AAA33266.1; ALT_TERM. EMBL; M23754; AAA33268.1; ALT_TERM. EMBL; M23754; AAA33268.1; ALT_TERM. EMBL; M23754; AAA33268.1; ALT_TERM. EMBL; M23754; AAA33268.1; ALT_TERM.
                                                                                                  MEDLINE-89352609; PubMed-2548604;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00348; UBIQUITIN.
PROSITE; PS00299; UBIQUITIN_1; 1.
PROSITE; PS50053; UBIQUITIN_2; 1.
                                                           FEBS Lett. 229:273-278(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nuclear protein; Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                    SEQUENCE OF 13-76 FROM N.A.
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PIR, B27806; B27806.
PIR, A34080; A34080.
PIR, B34080; B34080.
PIR; C34080; C34080.
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SEQUENCE FROM N.A.
                                                                                                                                                                            SEQUENCE FROM N.A.
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PIR; E34080;
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-!- FUNCTION: SAM (SUBSTRATE-ADHESTON MOLECULE) THAT APPEARS TO INHIBIT CELL MIGRATION. MAY PLAY A ROLE IN SUPPORTING THE GROWTH OF EPTTHELIAL TUMORS.
-!- SUBUNIT: HEXAMERIC. A HOMOTRIMER MAY BE FORMED IN THE TRIPLE COLLED-COLIL RESIDNA AND MAY BE STABILIZED BY DISULFIDE RINGS AT BOTH ENDS. TWO OF SUCH HALF-HEXABRACHIONS MAY BE DISULFIDE LINKED WITHIN THE CENTRAL GLOBULE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 464-1018 AND 1412-1661 FROM N.A., AND SEQUENCE OF 852-868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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-!- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 230 KDA (SHOWN HERE), 200 KDA
AND 190 KDA, ARE PRODUCTD BY ALTERNATIVE SPLICING. THEY ARE
PRODUCED IN A TISSUE-AND TIME-SPECIFIC MANNER DURING DEVELOPMENT.
-!- INDUCTION: BY TGF-BETA.
-!- SIMILARITY: CONTAINS 13.5 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 11. FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS A DOMAIN RELATED TO THE C-TERMINAL PART OF
                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TENA_CHICK STANDARD;
PRT; 1808 AA.
P10039; P1313; O73584; O73585;
01-MAR-1999 (Rel. 10, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-OCT-2000 (Rel. 40, Last sequence update)
TENARSCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN)
GMEM) (J1) (MIOTENDINOUS ANTIGEN) (GLIOMA-ASSOCIATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225).
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MEDLINE-88176910; PubMed-2451243;
Jones F.S., Burgoon M.P., Hoffman.S., Crossin K.L., Cunningham B.A.,
Edelman G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A cDNA clone for cytotactin contains sequences similar to epidermal growth factor-like repeats and segments of fibronectin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spring J., Beck K., Chiquet Ehrismann R.; Two contrary functions of tenascin: dissection of the active sites by recombinant tenascin fragments.";
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MULTIUBIQUITIN ADDUCTS.
COUNDGATION TO ACCEPTOR PROTEINS.
K -> N (IN SOME CLONES REPEATS).
6427383968EA8A84 CRC64;
                                                                                                                                                                                   1; Length 76
                                                                                                                                                                                                                                                  7; Indels
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EMBO J. 7:2977-2982(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 27-722 FROM N.A., AND SEQUENCE OF 79-96
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                                                                                                                                                                                      ВВ
                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                      Score 43;
Pred. No.
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MEDLINE-89030589; PubMed-2460335;
Pearson C.A., Pearson D., Shibahara
Chiquet-Ehrismann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90030407; PubMed-2478295;
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11
8538 MW;
                                                                                                                                                                                      40.2%;
42.9%;
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                                                                                                                                                                                                                                                  9; Conservative
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                                                                                                                                                                                      Query Match
Best Local Similarity
                               76
11
76 AA;
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01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
SUPRESSOR OF TUMORIGENICITY 14 (EC 3.4.21.-) (MATRIPTASE) (MEMBRANE-
TYPE SERINE PROTEASE 1) (MT-SP1).
ST14 OR PRSS14 OR SNC19.
BY SIMILARITY.
BY SIM
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58.3%; Pred. No. 88;
ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F (IN REF. 3).
B924A06CF9EFD6DE CRC64;
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-> TEY (IN RE
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1087 ETWNITVPGGQH 1098
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Best Local Similarity
Matches 7; Conserv
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ST14_HUMAN
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     SEEPTAN
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                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00008; EGF; 13.
Pfam; PF00147; fibrinogen_C; 1.
Pfam; PF00141; fibrinogen_C; 1.
PROSITE; PS01022; EGF_1; 14.
PROSITE; PS01186; EGF_2; 14.
Glycoprotein; Cell adhesion; Repeat; EGF-like domain; Coiled coil;
Extracellular matrix; Signal; Alternative splicing.
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EGF-LIKE 1 (INCOMPLETE).

EGF-LIKE 3.

EGF-LIKE 3.

EGF-LIKE 4.

EGF-LIKE 5.

EGF-LIKE 6.

EGF-LIKE 9.

EGF-LIKE 10.

EGF-LIKE 11.

EGF-LIKE 11.
                                                                                                                                             EMEL; X08031; CAB40811.1; -...
EMBL; X08030; CAB30824.1; ALT_TERM.
EMBL; X08030; CAB30824.1; ALT_SEQ.
EMBL; M3091641; AAA48749.1; ALT_SEQ.
PIR; A310903; A31093.
PIR; A31930; A31930.
PIR; A31379; A31379.
PIR; S33779; B33779.
PIR; S03279; S03279.
PIR; S01292; S01292.
HSSP; P24821; ITEN.
                                                                                                                                 EMBL; M23121; AAA49086.1; -.
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Gaps

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EMBL; X60190; CAA42745.1; -. EMBL; X99960; CAA68214.1; -. EMBL; Z72670; CAA96860.1; -.
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                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                       STANDARD;
 603
851
656
711
805
109
302
485
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367 TWNIEVPNNQHV 378
                                                                                                                                                                              3 TFQVEVPGSQHI 14
                                                                                       772
855 AA;
                                                                                                                                  Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                   ARO2 OR YGL148W.
                                                                                                                                                                                                                                                                                                                         PHOSPHOLYASE)
                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-S288C
                                                                                                                                                                                                                                                      AROC_YEAST
P28777:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cerevisiae
                      ACT_SITE
ACT_SITE
ACT_SITE
CARBOHYD
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AROC_YEAST
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                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-99303581; PubMed-10373424;
Lin C.Y., Anders J., Johnson M., Sang Q.A., Dickson R.B.;
Lin C.Y., Anders J., Johnson M., Sang Q.A., Dickson R.B.;
Molecular cloning of cDNA for matriptase, a matrix-degrading serine protease with trypsin-like activity.";
J. Blol. Chem. 274:18231-18236(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                               SEQUENCE FROM N.A.

Takeuchi T., Shuman M.A., Craik C.S.;

Takeuchi T., Shuman M.A., Craik C.S.;

"Reverse blochemistry: Use of macromolecular protease inhibitors t dissect complex biological processes and identify a membrane-type serine protease in epithelial cancer and normal tissue.";

Proc. Natl. Acad. Sci. U.S.A. 96:11054-11061(1999).
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; DVI.3045. ...
RILGERPO; IPR0001254; -..
RILGERPO; IPR0001254; -..
RILGERPO; IPR001314; -..
RILGERPO; IPR001314; -..
RILGERPO; IPR001314; -..
REPIM: PF000657; LIQLECEPPL_a; 4..
REPIM: PF00089; trypsin; 1..
REPIM: PF00721; CHYMOTRYPSIN.
REPROSTIE; PS00134; TRRYPSIN.
REPROSTIE; PS00136; TRRYPSIN.
REPROSTIE; PS01195; TRRYPSIN.
REPROSTIE; PS01195; CHYMOTRYPSIN.
REPROSTIE; PS01196; CHEA.]; 2.
REPROSTIE; PS01068; LDLRA.]; 2.
REPROSTIE; PS01068; LDLRA.]; 3.
RESIGNAL anothor; Repeat.
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CUB 2.
LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF118224; AAD42765.2; -. EMBL; AF133086; AAF00109.1; -.
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334
447
487
524
560
  sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                          TRYPSIN FAMILY
                                                                                                                                                                                                             CHARACTERIZATION.
                                                                                                                                                                                                                                 PubMed-10373425;
                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- COFACTOR: REDUCED FLAVIN.
-!- PATHWAY: SEVENTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN
THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKLMATE PATHWAY).
-!- SUBUNIT: HOMOTETRAMER (EY SIMILMARITY).
-!- INDUCTION: BY AMINO ACID STARYATION.
-!- SIMILMARITY: BELONGS TO THE CHORISMATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHORISMATE SYNTHASE (EC 4.6.1.4) (5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-92114793; PubMed-1837329; Moose D.G.L., Reusser U., Braus G.H.; Molecular cloning, characterization and analysis of the regulation of the ARO2 gene, encoding chorismate synthase, of Saccharomyces
                                                      CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                               N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Pred. No. 57;
                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (P. 26143132C01F99C9 CRC64;
LDL-RECEPTOR CLASS A 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
                                 CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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50.0%;
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Query Match
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J. Inherit. Metab. Dis. 22:414-427(1999).
-!- CATALYTIC ACTIVITY: 4-AMINOBUTANOATE + 2-OXOGLUTARATE = SUCCINATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medina-Kauwe L.K., Tobin A.J., De Meirleir L., Jaeken J., Jakobs C.,
Nyhan W.L., Gibson K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 de Biase D., Barra D., Simmaco M., John R.A., Bossa F.;
"Primary structure and tissue distribution of human 4-aminobutyrate
aminotransferase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- TISSUE SPECIFICITY: LIVER > PANCREAS > BRAIN > KIDNEY > HEART >
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osei Y.D., Churchich J.E.; "Screening and sequence determination of a cDNA encoding the human
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- DISEASE: DEFECTS IN ABAT ARE A CAUSE OF GABA-AT DEFICIENCY PHENOTYPE INCLUDES PSYCHOMOTOR RETARDATION, HYPOTONIA,
                                                                                                                           Length 376;
                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
4-AMINOBUTYRATE AMINOTRANSFERASE, MITOCHOUDRIAL PRECURSOR (EC 2.6.1.19) (GAMMA-AMINO-N-BUTYRATE TRANSAMINASE) (GABA AMINOTRANSFERASE) (GABA-AT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPERREFLEXIA, LETHARGY, REFRACTORY SEIZURES, AND EEG
                                                                                                                                                  Indels
                                                                                         AF3AF65605B91E8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 368-465 FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                   4;
                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: MONOMER (PROBABLE).
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
                  InterPro; IPR000453;
Pfam; PF01264; Chorismate_synt; 1.
PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.
PROSITE; PS00788; CHORISMATE_SYNTHASE_2; 1.
PROSITE; PS00789; CHORISMATE_SYNTHASE_2; 1.
Lyase; Aromatic amino acid blosynthesis.
                                                                                                                                                                                                                                                       500 A.A.
                                                                                                                                                  1; Mismatches
                                                                                                                           Score 41.5;
Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4-aminobutyrate aminotransferase.";
                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99336116; PubMed=10407778;
                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Brain;
MEDLINE=95237607; PubMed=7721088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95154329; PubMed=7851425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEMIALDEHYDE + L-GLUTAMATE
                                                                                        40838 MW;
                                                                                                                          38.8%;
                                                                                                                         Query Match 38.8
Best Local Similarity 62.5
Matches 10; Conservative
                                                                                                                                                                                              258 GSGFQGVSVPGSKHND 273
                                                                                                                                                                        1 GETFQ-VEVPGSQHID 15
                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 155:185-187(1995).
          S0003116; ARO2
                                                                                         376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                       GABT_HUMAN
                                                                                        SEQUENCE
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                                                                                                                                                                                                                                RESULT 12
GABT_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Henrich B., Monnerjahn U., Plapp R.;
"Peptidase D gene (pepD) of Escherichia coli K-12: nucleotide
sequence, transcript mapping, and comparison with other peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T., Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S., Mizuno T., Makino K., Nakata A., Yura T., Sampei G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                           4-AMINOBUTIRATE AMINOTRANSFERASE.
PYRIDOXAL PHOSPHATE.
R -> K (IN GABA-AT DEFICIENCY; 25%
REDUCTION IN ACTIVITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                               Pfam; PF00202; aminotran_3; 1.
PROSITE; PS00600; AA_TRANSFER_CLASS_3; 1.
Transferase; Aminotransferase; Pyridoxal phosphate;
Neurotransmitter degradation; Mitochondrion; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 500;
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D -> H (IN REF. 2).

V -> L (IN REF. 2).

E -> G (IN REF. 2).

K -> Q (IN REF. 2).

W -> G (IN REF. 2).

S -> A (IN REF. 2).

G -> R (IN REF. 2).

G -> R (IN REF. 2).

C -> G (IN REF. 2).

L -> H (IN REF. 2).

W; 41199085693780AD CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41.5; I
Pred. No. 39;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                               MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Bacteriol. 172:4641-4651(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-90330577; PubMed-1695895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56557 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.8%;
55.6%;
                                                                                                                                                               EMBL; L32961; AAA74449.1; -.
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17 TYRLLVPGSRHI-SQAAA 33
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                                                                                                                                                                                                            InterPro; IPR000954; -.
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STRAIN-K12 / W3110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
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                                                                                                                                                                                                                                                                                                                          Disease mutation.
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Ichihara S.
Mizobuchi K
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Romier C., Reuter K., Suck D., Ficner R.;
"Crystal structure of tRNA-guanine transglycosylase: RNA modification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Graedler U., Gerber H.D., Goodencough Lashua D.M., Garcia G.A.G., Ficner R., Reuter K., Stubbs M.T., Klebe G.; "A new target for shigellosis: rational design and crystallographic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reuter K.K.H., Ficner R.; "Sequence analysis and overexpression of the Zymomonas mobilis tgt "Sequence analysis and overexpression of the Zymomonas mobilis tgt biochemical characterization of the enzyme."; J. Bacteriol. 177:5284-5288(1995).
                                                                                                                                                               Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases
-- SIMILARITY: SOME, TO YEAST YDLO87C AND S.POMBE SPCCI6All.13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt Zymomonas \ mobilis.} Bacteria; Proteobacteria; alpha subdivision; Sphingomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGT_ZYMMO STANDARD; PRT; 385 AA.
P28720; Q60247;
01-DEC-1992 (Rel. 24, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
OUEUINE TRNA-RIBOSYLFRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., SEQUENCE OF 1-6, AND CHARACTERIZATION MEDLINE=95394847; PubMed=7665516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    000D2327621BFED0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38.3%; Score 41; DB 46.2%; Pred. No. 28; Live 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.85 ANGSTROMS).
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FEMS Microbiol. Lett. 75:19-26(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE FROM N.A.
STRAIN-ATCC 31821 / 2M4 / CP4;
MEDLINE-92406015; Pubmed-1526462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U21317; AAA62527.1; -. WormPep; B0495.8; CE01766. Hypothetical protein. SEQUENCE 313 AA; 36977 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 15:2850-2857(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 EVPGSQHIDSQKK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 QLMGSQHVDNKEK 23
                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         by base exchange.
   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=542;
                                                                                                                                    Kirsten J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
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      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCOOR SERVING THE SERVING SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lbs.sib.ch).
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MGIRRK -> MLETETGRYSDTLRSALVSLDGDNAWALSES
MGIRRE -3 AND 4).
9D2EBD9AF7A04831 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DENTIFICATION OF PROTEIN.
MEDLINE-93027135; PubMed-1408743;
Pel H.J., Fep M., Grivell L.A.;
Sequence comparison of new protein and mitochondrial members of the polypeptide chain release factor family predicts a five-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE PROKARYOTIC AND MITOCHONDRIAL RELEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
SEQUENCE FROM N.A.
STARAIN-KIZ / MGIGS5;
MEDIJINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Rlley M., Collado-Yides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Res. 20:4423-4428(1992).
COULD BE PROTEIN FACTOR INVOLVED IN TRANSLATIONAL
                                                                                                                                                                                                                                                                                                                                           Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O. Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
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01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 37.0 KDA PROTEIN B0495.8 IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 AA
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Pred. No. 12;
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Mismatches
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EMBL; D83536; BAA77905.1; -.
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PROSITE; PS00745; RF_PROK_I; 1.
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EMBL; U70214; AAB08656.1;
Ecogene; EG11496; prfH.
InterPro; IPR000352;
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35.0%;
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Best Local Similarity 35.0%
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TERMINATION.
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009217;
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RESULT 14 YP68_CAEEL

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Lambda phage group.
NCBI_TaxID=10719;
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P08979;
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                                                       DEAZAGUANINE IN TRNAS WITH GU(N) ANTICODONS (TRNA-ASP, -ASN, -HIS AD-TYR). AFTER THIS EXCHANGE, A CYCLOPENTENDIOL MOIETY IS ATTACHED TO THE 7-AMINOMETHYL GROUP OF 7-DEAZAGUANINE, RESULTING IN THE HYPERMODIFIED NUCLEOSIDE QUEUOSINE (Q) (7-(((4,5-CIS-DITY))) ANTICOXY-2-CYCLOPENTEN-1-Y1)AMINO)METHYL) 7-DEAZAGUANOSINE). CATALYTIC ACTIVITY: TRNA GUANINE + QUEUINE = TRNA QUEUINE + GUANINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                               -1- SUBUNIT: MONOMER.
-1- SIMILARITY: BELONGS TO THE QUEUINE TRNA-RIBOSYLTRANSFERASE FAMII
-1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY DUE
studies of inhibitors of tRNA-guanine transglycosylase."; Submitted (MAR-2000) to the PDB data bank.
                                                                                                                                                                                           COFACTOR: BINDS AND REQUIRES ZINC FOR ACTIVITY. ALSO REQUIRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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01-OCT-1994 (Rel. 30, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HYPOTHETICAL 43.8 KDA PROYEIN IN XPAC-ABRB INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L3377; AAA27704.1; ALT_INIT.
EMBL; L33777; AAA27705.1; ALT_INIT.
EMBL; Z11910; ·; NOT_ANNOTATED_CDS.
PDB; 1PUD; 07-JUL.97.
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ZINC.
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MEDLINE=96051385; PubMed=7584024;
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07-JUL-97.
19-APR-00.
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Pfam; PF01702; TGT; 1.
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Best Local Similarity
'-hag 8; Conserve
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                                                                                                                                                                                                                                                                                         TO FRAMESHIFTS.
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ACT_SITE
METAL
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   SOUTH THE TEST SEARCH S
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                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-94374705; PubMed=8088546;
Hartley N.M., Murphy G.O., Bruton C.J., Chater K.F.;
"Sequence of the essential early region of phi C31, a temperate phage of Streptomyces spp. with unusual features in its lytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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"The repressor gene (c) of the Streptomyces temperate phage phi c31:
"The repressor gene (c) of the Streptomyces temperate phage phi c31:
nuclectide sequence, analysis and functional cloning.";
Mol. Gen. Genet. 213:269-277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae;
Ogasawara N., Nakai S., Yoshikawa H.; "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.3%; Score 41; DB 1; Length 386; 31.2%; Pred. No. 35; ive 8; Mismatches 3; Indels
                                                                                                                                                                                                                            Bookstein C., Edwards C.W., Hulett F.M.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E -> M (IN REF. 2).
D921F3A0F6845EEE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
10-NOV-1997 (Rel. 35, Last annotation update)
REPRESSOR PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       683 AA.
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MEDLINE=89039715; PubMed=3185504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                386 AA; 43830 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; D26185; BAA05262.1; -. EMBL; M96156; AAA22892.1; -.
                                                                                                                                                                                                SEQUENCE OF 1-191 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; 299104; CAB11802.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SubtiList; BG10090; yaaN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 31.2
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 VEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|:|||: ::|: : 22 IEIPGSEAVKAEKEQV 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                         Res. 1:1-14(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage phi-C31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 147:29-40(1994).
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PRINTS; PR00379; INTEIN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                          Thermococcus litoralis.
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus
NCBI_TaxID=2265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
-i- FUNCTION: INTEIN ENCODED ENDONUCLEASES ARE THOUGHT TO MEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE =
PROPER PROPER NORTH NUBERGOES A PROTEIN SELF SPLICING THAT INVOLVES
PRO: TRANSLATIONAL EXCISION OF THE TWO INVERVENING REGION
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTEIN MOBILITY BY SITE-SPECFIC RECOMBINATION INITIATED BY ENDONUCLEASE CLEAVAGE AT THE "HOMING SITE" IN GENE THAT LACK THE
                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-ARR-1993 (Rel. 25, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
DNA POLYMERASE (EC 2.7.7.7) (VENT DNA POLYMERASE) [CONTAINS: PI-TLI ENDONUCLEASE; PI-TLI II ENDONUCLEASE].
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDIINE-92302285; PubMed-1608969;
Perler F.B., Comb D.G., Jack W.E., Moran L.S., Qiang B.,
Kucera R.B., Benner J., Slatko B.E., Nwankwo D.O., Hempstead S.K.,
Carlow C.K.S., Jannasch H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN SPLICING.
MEDILIES-93117083; PubMed=1475179;
HOdges R.A., Perler F.B., Noren C.J., Jack W.E.;
"Protein splicing removes intervening sequences in archaea DNA
                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Intervening sequences in an Archaea DNA polymerase gene.";
Proc. Natl. Acad. Sci. U.S.A. 89:5577-5581(1992).
                                                                                             38.3%; Score 41; DB 1; Length 683; 50.0%; Pred. No. 65; ive 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INTEINS) FOLLOWED BY PEPTIDE LIGATION.
SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
EMBL; X12865; CAA331345.1; -.
EMBL; X76288; CAA53911.1; -.
PIK; S01433; S01433; S014434.
Transcription regulation; Repressor; DNA-binding.
SEQUENCE 683 AA; 74077 MW; B02379D204F37D1B CRC64;
                                                                                                                                                                                                                                           PRT; 1702 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 20:6153-6157(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M74198; AAA72100.1; -. EMBL; M74198; AAA72101.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00136; DNA_pol_B; 3.
                                                                                             Query Match 38.3
Best Local Similarity 50.0
Matches 7; Conservative
                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S42459; S42459.
REBASE; 2613; PI-T111.
REBASE; 2621; PI-T1111.
                                                                                                                                                 1 GETFQVEVPGSQHI 14
                                                                                                                                                                         86 GRIFDTELTGADHI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002064; -.
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P30317;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Thermococcus.
NCBL_TaxID=86030;
                                                                                                                           DNA POLYMERASE, 1ST PART.
PI-TLI II ENDONUCLEASE (TLI POL-1 INTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 204:153-158(1997).
--- CATALYTIC ACTIVITY. N DEOXYNUCLEOSIDE TRIPHOSPHATE --
N PYROPHOSPHATE + DNR(N).
--- PTM: THIS PROPEIN UNDERGOES A PROTEIN SELE SPLICING THAT INVOLVES
A POST-TRANSLATIONAL EXCISION OF THE THREE INTERVENING REGION
(INPEINS) FOLLOWED BY PEPTIDE LIGATION.
--- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                   DNA POLYMERASE, 2ND PART.
PI-TLI I ENDONUCLEASE (TLI POL-2 INTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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INTEIN II.
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InterPro: IPR002203: -.
Pfam. PF00136; DNA_pol_B; 4.
PROSITE; PR00379; INTERN.
PROSITE; PS00116; DNA_POLYMERASE_B; FALSE_NEG.
PROSITE; PS00181; PROTEIN_SPLIGING;
TAGASTE; PS00481; PROTEIN_SPLIGING;
DNA_binding; Hydrolase; Endonuclease; Autocatalytic cleavage;
PROSITE; PS00116; DNA_POLYMERASE_B; FALSE_NEG.
PROSITE; PS00881; PROTEIN_SPLICING; 2.
Transferase; DNA-directed Dymerase; DNA replication;
DNA-binding; Hydrolase; Endonuclease; Autocatalytic cleavage;
                                                                                                                                                                                                                                                                                                                                                                       Length 1702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Niehaus F., Frey B., Antranikian G.; "Cloning and characterisation of a thermostable alpha-DNA | from the hyperthermophilic archaeon Thermococcus sp. TY."; Gene 204:153-158(1997).
                                                                                                                                                                                                                                                                                                                                                Score 41; DB 1; Lengtn 1, 2, 2, Pred. No. 1, Pe+02;
                                                                                                                                                                                                                                                                             DNA POLYMERASE, 3RD PART. W; 21D6B98C75F53B20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1829 AA
                                                                                                                                                                                                                                                                                                                                                                                                                          3; Mismatches
                                                                                                                                                                                                                                                   (IVPS2)
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                                                                                                                                                                                                                                                                                                                                                                         38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA POLYMERASE (EC 2.7.7.7).
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Best Local Similarity 40...
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 GDSFAVEIKGRIHFD 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GETFQVEVPGSQHID 15
                                                                                                                           494
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1471
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769
855
1392
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                                                                                                      Protein splicing.
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                                                                                                                                     495
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770
856
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033845;
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a iiii

d.

B60A605222CBBCAC CRC64;

95797 MW;

862 AA;

SEQUENCE

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BY SEQUENCE FROM N.A.

BY SEAL STATE OF STA
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  POLYMERASE, 3RD PART (POTENTIAL).
                        INTEIN III.
DNA POLYMERASE, 4TH PART (POTENTIAL).
W; All3A8BC57EB9CB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

ISSUB-Endometrial tumor;

MEDLINE-94352394; Pubmed-8072530;

Nicolaides N.C., Papadopoulos N., Liu B., Wei Y.-F., Carter K.C.,
Ruben S.M., Rosen C.A., Haseltine W.H., Fleischmann R.D.,
Fraser C.M., Adams M.D., Venter J.C., Dunlop M.G., Hamilton S.R.,
Petersen G.M., de la Chapelle A., Vogelstein B., Kinzler K.W.;

"Mutations of two PMS homologues in hereditary nonpolyposis colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PMS1 PROTEIN HOMOLOG 2 (DNA MISMATCH REPAIR PROTEIN PMS2).
                                                                                                                                                   Score 41; DB 1; Length 182
Pred. No. 1.9e+02;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /FTId-VAR_004469.
P -> S (IN REF. 2)
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01-OCT-1996 (Rel. 34, Last sequ
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                                                                                                                                                     38.3%;
46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U13696; AAA63923.1; -.
                                                                          211875
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                        1 GETFQVEVPGSQHID 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer.";
Nature 371:75-80(1994).
1441
                                                  1829
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                ¥.
                                                                                                                                                     Query Match
Best Local Similarity
1393
1442
1599
1829
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                                                CHAIN
SEQUENCE
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                        CHAIN
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FFFS
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                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ST. LAWRENCE 74 / SL 74 / ORS 6A;
MEDLINE-8936647; PubMed=2549509;
Tacciol1 G.E., Grotewold E., Aisemberg G.O., Judewicz N.D.;
"Ubiquitin expression in Neurospora crassa: cloning and sequencing of a polyubiquitin gene.";
Nucleic Acids Res. 17:6153-6165(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-ST. LAWRENCE 74 / SL 74 / ORS 6A;
MEDLINE-91323720; PubMed=1650731;
Taccioli G.E., Grotewold E., Alsemberg G.O., Judewicz D.N.;
The cDNA sequence and expression of an ubiquitin-tail gene fusion in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 147:137-140(1994).
-!- FUNCTION: INVOLVED IN THE ATP-DEPENDENT SELECTIVE DEGRADATION OF CELLULAR PROTEINS, THE MAINTENANCE OF CHROMATIN STRUCTURE, THE REGULATION OF GENE EXPRESSION, THE STRESS RESPONSE, AND RIBOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANDOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN PRECURSON WITH 4 EXACT HEAD TO TAIL REPEATS. THERE IS A FINAL AMINO-ACID (ELN) AFTER THE LAST REPRAT. SOME UBIQUITIN GENES CONTAIN A SINGLE COPY OF UBIQUITIN FUSED TO A RIBOSOMAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=74-OR23-1A;
MEDLINE-94374698; PubMed-8088539;
Tarawneh K.A., Anumula K.R., Free S.J.;
"The isolation and characterization of a Neurospora crassa gene (ubi::crp-6) encoding a ubiquitin-40S ribosomal protein fusion protein.";
                                      1;
                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
   Length 862;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOGENESIS.
SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
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Score 40.5; DB 1;
Pred. No. 1e+02;
2; Mismatches 0;
                                                                                                                                                                                                                              01-3AN-1990 (Rel. 13, Created)
01-3AN-1990 (Rel. 13, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                  76 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X13140; CAA31530.1; ALT_TERM.
EMBL; U01220; AAA56880.1; ALT_TERM.
PIR; S05323; UQNC.
PIRSP; P02248; DAR.
InterPro; IPR000626; -.
 37.9%;
75.0%;
                                     9; Conservative
                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurospora crassa.";
Gene 102:133-137(1991).
                                                                                          10 GSQ-HIDSQKKA 20
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                            Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                  UBIO_NEUCR
                                                                                                                                                                                                                                                                                       UBIQUITIN.
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                                                                                                                                                             KESULT 21
UBIQ_NEUCR
                                     Matches
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PRINTS; PR00348; UBIQUITIN.
PROSITE; PS00299; UBIQUITIN_1; 1.
PROSITE; PS50053; UBIQUITIN_2; 1.
Mon Jul 16 16:58:13 2001
                                                                                                                         Nuclear protein; Polyprotein.
                                                                     Pfam; PF00240; ubiquitin; 1.
                                                                                                                                       SITE
                                                                     DR DR DR DR DR SS FT FT SS
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NECESSARY FOR BRANCHED-CHAIN MULTIUBROUTIN ADDUCTS. CONJUGATION TO ACCEPTOR PROTEINS. 994480FE7D38403E CRC64; 37.4%; Score 40; DB 1; Length 76; 42.9%; Pred. No. 9; tive 4; Mismatches 8; Indels 1 GETFQVEVPGSQHIDSQKKAI 21 76 76 76 AA; 8598 MW; Query Match
Best Local Similarity 42.9
Matches 9; Conservative SEQUENCE BINDING ö

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Gaps

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10 GKTITLEVESSDTIDNVKQKI 30 셤

30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) TRANSLATION INITIATION FACTOR 5A (EIF-5A) (HYPUSINE-CONTAINING PRT; STANDARD; EIF5A OR APE2085. IF5A_AERPE Q9YA53; IF5A_AERPE 

148

Aeropyrum pernix. Archaea; Crenarchaeota; Desulfurococcales; Desulfurococcaceae; SEQUENCE FROM N.A NCBI_TaxID=56636; Aeropyrum.

MEDLINE-99310339; PubMed-10382966;

Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y., Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi Hosoyama R., Fukui S., Nagai Y., Nishijima K., Nakazawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi M., Aoki K.-I., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Romura Y., Nomura N., Sako Y., Kikuchi H.; Romura Y., Romura Y., Alamani A., Aoki M., Aoki M., Romura Y., Nomura N., Sako Y., Kikuchi H.;

Ή.

crenarchaeon, Aeropyrum pernix Kl."; DNA Res. 6:83-101(1999).

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(See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch)

50 50 HYPUSINE (BY SIMILARITY). 148 AA; 16205 MW; B7C886047F0FB46F CRC64; EMBL; Arverson InterPro; IPR001884; -. InterPro; IPR001884; -. Pfan; PF01287; -- PF5A; HYPUSINE; I. PROSITE; FS00302; IF5A; HYPUSINE; I. Frownthesis; Initiation factor; Hypusine. The Property of Pro EMBL; AP000063; BAA81096.1; -. MOD_RES SEQUENCE

Gaps ö 37.4%; Score 40; DB 1; Length 148; 42.1%; Pred. No. 18; 8; Indels 3; Mismatches Query Match 37.4%; Best Local Similarity 42.1%; Matches 8; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage by and for commercial
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LÒCATIÓN: ENDOPLASMIC RETICULUM LUMEN.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY. STRONG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00014; ER_TARGET; 1.
PROSITE; PS00297; HSP70_1; PARTIAL.
PROSITE; PS00329; HSP70_2; PARTIAL.
PROSITE; PS01035; HSP70_3; PARTIAL.
ATP-binding; Heat shock; Endoplasmic reticulum; Multigene family.
                                                                                                                                                                                                                                                                                                                                                         Heschl M.F.P., Baillie D.L.; "Identification of a heat-shock pseudogene from Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              285 288 PREVENT SECRETION FROM ER 288 AA; 31267 MW; 967F5A4A12FA67BF CRC64;
                                                                                                                                                01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HEAT SHOCK 70 KDA PROTEIN D (FRAGMENT).
                                                                                                                  288 AA
                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-89306577; Pubmed-2744444;
                 :||:|| || : | |
103 DTFEVEKPGGNEEEEQLAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M28528; AAA28076.1; -.
ETFQVEVPGSQHIDSQKKA 20
                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             Genome 32:190-195(1989).
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InterPro; IPR001023; -.
Pfam; PF00012; HSP70; 1
PROSITE; PS00014; ER_TAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TO MAMMALIAN GRP78.
                                                                                                                                                                                                                                     Caenorhabditis elegans
                                                                                                                                                                                                                                                                                       NCBI_TaxID-6239;
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                                                                                                                HS74_CAEEL
P20163;
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Gaps ; Length 288; 5; Indels 1; DB 37; Mismatches Score 40; Pred. No. 3 9 37.4%; Conservative Ouery Match Best Local Similarity 6; Conserva'

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| | :::| | |:::| | 133 TFEIDVNGILHVSAEDK 149 3 TFQVEVPGSQHIDSQKK 19

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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 39.9 KDA PROTEIN 715H9.1 IN CHROMOSOME II PRECURSOR. PRT; STANDARD; YRY1_CAEEL Q10005; 01-NOV-1997 ( 01-NOV-1997 ( RESULT 24 

355 AA

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. T15H9.1. Caenorhabditis elegans

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-!- FUNCTION: NADP+(-)DEPENDENT ADH ACTIVITY.
-!- CATALYTIC ACTIVITY: AN ALCOHOL + NADP(+) = AN ALDEHYDE OR KETONE +
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Matches
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                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Cloning and expression of a putative alcohol dehydrogenase gene of Entamoeba histolytica and its application to immunological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
HYPOTHETICAL PROTEIN T15H9.1.
J-DOMAIN.
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                                                                                                                                      Gardner A.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 1 J DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95FA4D8E551D9CC2 CRC64;
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Nakabayashi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagn. Lab. Immunol. 3:270-274(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOZIMPEP; T15H9.1; CE01664.
INTERPRO; IPR001623; -
InterPro; IPR002939; -
Pfam; PF00256; DnaJ; 1.
Pfam; PF01556; DnaJ_C; 1.
PROSITE; PS00636; DNA__1; 1.
HYPOTHETICAL PROSITE; PS50076; DNAJ_Z; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.4%; Score 40; DB
llarity 47.4%; Pred. No. 47;
Conservative 2; Mismatches
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Eukaryota, Entamoebidae, Entamoeba.
NCBI_TaxID=5759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-HM-1:IMSS;
MEDLINE-96201701; PubMed-8611619;
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MEDLINE-96336080; PubMed-8705667;
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Best Local Similarity
Matches 9; Conserv
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                                                                                                        STRAIN=BRISTOL N2;
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                                                                       SEQUENCE FROM N.A.
NCBI_TaxID=6239;
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NAME OF THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
-!- SIMILARITY: BELONGS TO THE IRON-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R -> I (IN REF. 2).
TLENHQDY -> HKKIIKTI (IN REF. 2).
MISSING (IN REF. 2).
WNR -> NE (IN REF. 2).
; 506FBBA933631FA9 CRC64;
                      FAMILY; MOST SIMILAR TO C.ACETOBUTYLICUM BDHA AND BDHB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 1; Length 395;
Pred. No. 52;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                             Pfan; PF00465; Fe-ADH; 2.
PROSITE; PS00913; ADH_IRON_1; FALSE_NEG
PROSITE; PS00060; ADH_IRON_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: July 16, 2001, 16:44:05 Job time: 464 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43485 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 GETLAITTPGVMRFNKEKNA 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37.4%;
                                                                                                                                                                                                                                                                                     EMBL; D49910; BAA08651.1; -. EMBL; Z48752; CAA88639.1; -. InterPro; IPR001670; -.
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235
273
307
395 AA;
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Best Local Similarity
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Q9qz17 mus musculu
Q9u3m9 caenorhabdi
Q9u186 ovis aries
P97431 mus musculu
Q9p5z5 neurospora
Q9skb2 arabidopsis
Q9nf4 arabidopsis
Q9sn44 arabidopsis
                                                                         09qmn7 hepatitis b
090995 gallus gall
090824 gallus gall
090824 gallus gall
09120 pseudomonas
09135 homo sapien
091380 homo sapien
091380 homo sapien
055583 synechocyst
03135 bacillus ce
036581 mus musculu
096955 mus musculu
                                                                                                                                                                                          Q9mal6 arabidopsis
O70057 bordetella
                                                                                                                                                                                                                    Q9f517 zymomonas m
O04636 arabidopsis
Q9sq79 pinus taeda
                                                                                                                                                                                                           Q43098 psophocarpu
                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
STRAILNE-LASSICAL STRAIN 569B;
STRAILNE-91355224; PubMed=1883840;
Dams E., De Wolf M., Dierick W.;
"Nucleotide sequence analysis of the CT operon of the Vibrio cholerae classical strain 569B.";
Biochim. Biophys. Acta 1090:139-141(1991).
                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
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CHOLERA TOXIN B PROTEIN (CTB).
D6BF83FFF7924EA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xu L.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X58785; CAA41591.1; -.
EMBL; U25679; AA34728.1; -.
EMBL; A00931; CAA00098.1; -.
HSSP; P01556; 2CHB.
                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERA TOXIN B PROTEIN (CTB) PRECURSOR (CTB).
                                                                                                                                                                                                                                                                                                                   124 AA
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                                                                                                                                                                     Q9EPB5
Q9V9U6
Q9MA16
O70057
                                                                           Q9QMN7
Q90995
Q90824
Q9HTA0
Q9HB36
Q9HB36
Q9HCA3
Q9HCA3
Q9H330
Q9H335
         Q9U3M9
Q9N136
P97431
Q9P5Z5
Q9SKB2
                                                        Q9NF90
Q9SN44
                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CLASSICAL BIOTYPE 569B;
Shi C., Cao C., Zhang J., Ma Q.;
Chin. Biochem. J. 9:395-399(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001835; -.
Pfam; PR01376; EnterCtoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
PRODOM; PD012805; -; 1.
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124 CH
13919 MW;
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STRAIN=CLASSICAL BIOTYPE 569B;
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                            15.61
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22
124 AA;
  Vibrio cholerae.
  CHAIN
SEQUENCE
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Q57193;
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SIGNAL
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Q57193
  Q57193 vibrio chol
Q57635 vibrio chol
Q97615 vibrio chol
Q97646 vibrio chol
Q99987 homo sapien
Q91jb0 arabidopsis
Q91gm2 oryza sativ
Q40742 oryza sativ
Q9746 drosophila
Q9874 arabidopsis
Q9874 arabidopsis
Q9874 arabidopsis
Q9876 arabidopsis
Q91467 arabidopsis
Q9147 arabidopsis
Q9147 arabidopsis
Q9147 arabidopsis
Q91487 arabidopsis
Q9147 arabidopsis
Q9141 within hepa
                                                               July 16, 2001, 16:43:38; Search time 57.41 Seconds (without alignments) 48.396 Million cell updates/sec
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                                                                                                                                                                                          425026
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                        hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                               OM protein - protein search, using sw model
                                                                                                                        1 GETFQVEVPGSQHIDSQKKAI 21
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09LJB0
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09SXC9
09P4E0
09LY67
09J3F2
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Q9J3E8
Q22511
Q49876
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Q9RP15
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sp_rodent:*
sp_unclassified:*
sp_vertebrate:*
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sp_human:*
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45.5

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44 44 45 44 44

Minimum DB seq Maximum DB seq

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Perfect score:

Title:

Run on:

Scoring table: Sequence:

Searched:

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Homo sapiens (Human)
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBL_TaxID=666;
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STRAIN=KNIH002;
Shin H.J., Park Y.C., Kim Y.C.;
Shin H.J., Park Y.C., Kim Y.C.;
Cloning and nucleotide sequence analysis of the virulence gene cassette from Vibrio cholerae KNIH002 isolated in Korea.";
Misainmurhag Hoiji 35:205-210(1999).
EMBL: AFI75708; AAD51360.1; -.
HSSP; P01556; 2CHB.
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Yamamoto K., Do V.G., Xu M., Iida T., Miwatani T., Albert M.J.
                                                     94.4%; Score 101; DB 2; Length 124; 95.2%; Pred. No. 7.3e-09; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.4%; Score 101; DB 2; Length 124; 95.2%; Pred. No. 7.3e-09; 1ve 0; Mismatches 1; Indels
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3F87B2F297953179 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERA ENTEROTOXIN B-SUBUNIT.
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Last annotation update)
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Pfam; PF00176; EnterOtoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
PRODOM; PD012805; -; 1.
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SEQUENCE 124 AA; 13871 MW;
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                                                                                                                 Conservative
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Matches 20; Conserv
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                      Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Nakashima K., Eguchi Y., Nakasone N.;
"Characterization of an enterotoxin produced by Vibrio cholerae
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                                                                                                         Length 124;
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-!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL; AB000450; BAA19109.1; -.
HSSP; O60486; LCKI.
InterPro; IPR000719; -.
                                                                                                                                                      1; Indels
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PRINTS; PR00772; ENTEROTOXINB.
SEQUENCE 124 AA; 13905 MW; 23BF83FFF793E5B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2000 (TrEMBLrel. 15, Last annotation update)
CHOLERA-LIKE ENTEROTOXIN B SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                       Score 101; DB 2;
Pred. No. 7.3e-09;
0; Mismatches 1;
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                                                                                                         Query Match 94.4%;
Best Local Similarity 95.2%;
Matches 20; Conservative
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Best Local Similarity 90.5
Matches 19; Conservative
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PAC

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Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0041E11.";
                                                                                                                              Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
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                STRAIN-CV. NIPPONBARE;
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Q40742;
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                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicales; Arabidopsis.
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2005 (SZ0908).
01-YZA SAUTIVA (Rice).
01-YZA SAUTIVA (Rice).
EUKATYOTA: VIridiplantae: Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tabata S.;
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Pred. No. 3.2;
InterPro; IPR002290; -.
PRDM; PR00669; PKINASE. 2.
PROSTTE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_SI; 1.
AMART; SM00220; S_TKC; 1.
AMP-binding; Serime/threonine-protein kinase; Transferase.
SEQUENCE 508 AA; 58126 MW; 157FBF8F48511AF4 CRC64;
                                                                                                                                                                                                                                                                                50.5%; Score 54; DB 4; Length 508, 50.0%; Pred. No. 1.4; 7; Indels ive 3; Mismatches 7; Indels
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Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Ta
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Res. 7:217-221(2000).
EMBL; AP000606; BAB01195.1; -.
SEQUENCE 552 Aa; 63036 MW; 740EA16CDEBB2447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
EMB|CAB7996.1.
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Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 QVEIPASMEIDEETKAI 163
                                                                                                                                                                                                                                                                                                                 Best Local Similarity 50.0
Matches 10; Conservative
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SEQUENCE FROM N.A.
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PubMed-10907853;
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Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
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SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC clone:P0433F09.";
                                                                                                                                                                                                                                                                                                          Score 49; DB 10; Length 428;
Pred. No. 7.4;
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                                                                                                                                                                                                                                                                                                                                                          7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schultz T.F., Quatrano R.S.; "Characterization and expression of a rice RAD23 gene."; Plant Mol. Biol. 34:557-562(1997). EMB: UG5530; AAB65841.1; -. HSSP; P02248; ITBE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                           Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AP0002521; BAA96762.1; -. InterPro; IPR001552; -. Pfam; PF00441; Acyl-CoA_dh; 1. PR00451E; PS00441; Acyl-CoA_dh; 1. SEQUENCE 428 AA, 46132 MW; 8D34E3698ABE6367 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 AA
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Pred. No. 14;
4; Mismatches
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last anno
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STRAIN-NIPPONBARE;
MEDLINE-97369378; PubMed-9225866;
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InterPro; IPR000449; -:
InterPro; IPR000626; -:
Pfam; PF0020; ubiquitin; 1.
Pfam; PF00627; UBA; 2.
PROSITE; PS50053; UBIQUITIN_2; 1.
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10 GSTFQIEVDSAQKVADVKRII
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Best Local Similarity 42.9
Matches 9; Conservative
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Submitted (APR-1999) to the EMBL; AC006577; AAA25769.1; InterPro; IPR000626; -. Pfam; PF00240; ubiquitin; 2. SEQUENCE 91 AA; 10142 MW;
                                                                                                  Query Match
Best Local Similarity 47.6
Matches 10; Conservative
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Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                         09SXC9;
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                                                                                                                                                                                                                               RESULT 11
Q9SXC9
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                                                                                                                                                                                                                                                                                                                                                                  Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
Zieran L.L., Rubin G.M.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003408; AAF4447.l;
FlyBase: FBgn0028907; BG:DS01514.3.
                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                     Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";
Genetics 153:179-219(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. COLUMBIA,
Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Li J., Kremenetskala I., Luros J., Ngan I., Gonzalez A., Altafi H.,
Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Hulzar L., Kim C., Palm C., Rowley D., Shinn P., Walker M.,
Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"Arabidopsis thaliana chromosome 1 BAC F1511 sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Bragnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                              Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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Pred. No. 14;
2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .l protein.
395 Aa; 43561 MW; AE4F1CC4ADD3DA73 CRC64;
                          01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 43.6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 AA.
                -OCT-2000 (TrEMBLrel. 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-Y, CN BW SP;
MEDLINE-99403001; PubMed-10471707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.9%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-007-2000 (TrEMBLrel. 15,
F1511.6 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 56.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 QVEVPGSQHIDSQKKA 20
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                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-Y, CN BW SP;
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                                                                      BG:DS01514.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
SEQUENCE 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09SYF4;
09NKD5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9SYF4
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Q9SYF4
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SEQUENCE FROM N.A.

STRAIN-CV. COLUMBIA;

Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,

Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,

Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,

Chin C., Howng B., Choi E., Chiou J., Altafi H., Araujo R., Brooks S.,

Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,

Hizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P., Walker M.,

Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;

"Arabidopsis thaliana chromosome 1 BAC T17H3 sequence.";

Submitted (AuG-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, ACO05916; AAD45990.1;

InterPro; IPR001382;

Pfam. PF01323; Glycolhydro_477;

Dram.
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                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bagnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Eukaryota, Fungl; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 574;
                                                                                                                                                                                                       Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                    8; Indels
EMBL/GenBank/DDBJ databases
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A; 65707 MW; 4ACC456DE487EA93 CRC64;
                                                                                                                    E8766823D6450267 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
T17H3.2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) PHEROMONE-RESPONSIVE MAPKK KINASE UBC4.
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                                                                                                                                                                                                    Score 46; DB 10;
Pred. No. 4.3;
3; Mismatches 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 1
Pred. No. 31;
2; Mismatches
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01-0CT-2000 (TrEMBLrel. 15, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
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ب
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                                                                                                                                                                                                                                                                                                                                                                                   58 GKTFNLEVKGSEIIQQVKNMI 78
                                                                                                                 10142 MW;
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2732 AA

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Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., Lavi E.; "Pathogenesis and sequence analysis of mouse hepatitis virus type 2; an experimental model system of acute meningitis and hepatitis in
                                                                                                                                                                Viruses; SsRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-MHV-A59;
Leparc-Goffart I., Hingley S.T., Chua M.M., Jiang X., Lavl E.,
Weiss S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 45; DB 14; Length 2732;
Pred. No. 2.4e+02;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                         EMBL, AF208066; AAF69332.1; -. RNA-directed RNA polymerase. SEQUENCE 2732 AA; 309135 MW; 46D0385DE231DC49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Weiss S.R., Leparc-Goffart I., Hingley S.T.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 74029248; AAB8681B.1; -.
SRNA-directed RNA polymerase.
SEQUENCE 2733 AA; 309126 NW; 41A96EB2E2316CD9 CRC64;
                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ databases
                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
RNA-DIRECTED RNA POLYMERASE.
murine hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                           PRT;
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52.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.1%;
                                                                                                                                                                                                                                                                                                                         mice.";
Submitted (NOV-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA-DIRECTED RNA POLYMERASE murine hepatitis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.50,
Local 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1197 ETFONNVPNYQHIGMKR 1213
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                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virology 0:0-0(1997).
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Matches 9; Conserv
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                    NCBI_TaxID=11138;
                                                                                                                                                                                                                                                       STRAIN=PENN 97-1;
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                                                             Q9J3F2
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                                           09J3F2
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039226
       RESULT
09J3F2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Rieger M., Mewes H.W., Rudd Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.; Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                  SMART; SM00220; S_TKC; 1.—
ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SEQUENCE 1166 AA; 123298 MW; A89E0019AABD4172 CRC64;
Andrews D.L., Egan J.D., Mayorga M.E., Gold S.E.;
Andrews D.L., Egan J.D., Mayorga M.E., Gold S.E.;
The Ustilago maydis ubc4 and ubc5 genes encode members of a MAP
kinase cascade required for filamentous growth.";
Mol. Plant Microbe Interact. 13:781-786(2000).
I. SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL, AR197562; AAR86841.1;
InterPro; IPR000104;
InterPro; IPR000159;
                                                                                                                                                                                                                                                                                                                                                                                                              1;
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                                                                                                                                                                                                                                                                                                                                                                           3; Length 1166;
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ALI63818; CAB87801.1; -.
InterPro; IPR001752; -.
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ATP-binding; Coiled coil; Microtubules; Motor protein.
SEQUENCE 439 AA; 49028 MW; 9BD55085A1966D70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0c7-2000 (TrEMBLrel. 15, Created)
01-0c7-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
KINESIN HENY CHAIN-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                              4;
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                                                                                                                                                                                                                                                                                                                                                                           Score 45.5; DB
Pred. No. 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Profits: Prof. Kinesin; 2.
PRINTS: PR00380; KINESINHEAVY.
PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.1%; Score 45; DB 38.1%; Pred. No. 34;
                                                                                                                                                                                                           PRINTS, PR00308; ANTIFREEZEI.
PROSITE; PS00107; PROTEIL_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                              4;
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                                                                                                                                                                                                                                                                                                                                                                           42.5%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GETFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                             5 QVEVP-GSQHIDSQKKAI 21
                                                                                                                                                                                                pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.0°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 42.1
Best Local Similarity 38.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                              InterPro; IPR000719; -.
InterPro; IPR002290; -.
Pfam; PF00069; pkinase;
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RESULT 13

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O COLX 67 O COLX

2733 AA.

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Gaps

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Score 45; DB 14; Length 2733;
Pred. No. 2.4e+02;
2; Mismatches 6; Indels
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Q9PYA2
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ò g 1198 ETFONNVPNYQHIGMKR 1214

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PRT; 2733 AA

PRELIMINARY;

```
Rodrigues-Pousada C.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Vitaceae; Vitis.
NCBI_TaxID=29760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-1998 (TrEMBLrel. 16, Last annotation update)
CLASS III CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lupinus albus (White lupine).
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Paplilionoideae; Lupinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: FAD (BY SIMILARITY).
-!- SIMILARITY: TO PYRIDINE NUCLEOTIDE-DISULPHIDE OXIDOREDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; Interp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CV. THOMPSON SEEDLESS (CLONE 2A); TISSUE-FRUIT;
Cassol T., Adams D.O.;
                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GLUTATHIONE REDUCTASE (NADPH) (EC 1.6.4.2) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CV. ULTRA;
Regalado A.P., Vidal S., Neves A., Ricardo C.P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                           565 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44.5; Dl
Pred. No. 53;
2; Mismatches
                                                                                                                                                                                                  Created)
                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00390; IALG.
Mendel; 26381; Vitvi;1190;26381.
InterPro; IPR000103; -
InterPro; IPR001100; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF019907; AAB70837.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.6%;
58.8%;
                                                                                                                                                                                                  (TrEMBLrel. 05,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          233 GRPFIPEIPGSEHAIDS 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GETFQVEVPGSQH-IDS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 41.6
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                Vitis vinifera (Grape).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3870;
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                                                                                                                                                                                                  01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 049876
                                                                                                                                     022511
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049876
                                                                              RESULT
022511
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                                                                                                                                                                                                                                                                                                                                                                   SPECIES-murine hepatitis virus strain 2; STRAIN-MHV-2; Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., Lavi E.; "Pathogenesis and sequence analysis of mouse hepatitis virus type 2: an experimental model system of acute meningitis and hepatitis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=murine hepatitis virus strain ML-11; STRAIN=ML-11; Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., Lavi E.; "Pathogenesis and sequence analysis of mouse hepatitis virus type 2; an experimental model system of acute meningitis and hepatitis in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
RNA-DIRECTED RNA POLYMERASE.
murine hepatitis virus.
Viruses; ssrNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                            murine hepatitis virus, and murine hepatitis virus strain ML-11. Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; COTONAVIRIDAE; COTONAVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42.1%; Score 45; DB 14; Length 2733; 52.9%; Pred. No. 2.4e+02;
Live 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309420 MW; D04F6457578EC1E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF208067; AAF66342.1; -.
RNA-directed RNA polymerase.
SEQUENCE 2733 AA; 309251 MW; 47049486732FBAFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF201929; AAF19384.1; -.
EMBL; AF207902; AAF68920.1; -.
UL-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0RF1B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RNA-directed RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1198 ETFONNVPNYOHIGMKR 1214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ETFQVEVPGSQHIDSQK 18
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                                                                                                                                                                                                                                                                                 NCBI_TaxID=11138, 123595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2733 AA;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Q9J3E8 Q9J3E8; RESULT 17 Q9J3E8

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Gaps

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Length 565; Indels

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Mus musculus (Mouse).
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Matches 7; Conserv
                                                                                                                                    SEQUENCE FROM N.A.
                                                  SEQUENCE FROM N.A.
             NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9940;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P97431
P97431;
                                                                           White S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09N136
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P97431
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                Query Match
41.1%; Score 44; DB 10; Length 293;
Best Local Similarity 38.1%; Pred. No. 32;
Matches 8; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.1%; Score 44; DB 11; Length 330;
41.2%; Pred. No. 36;
ative 6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sands A., Mak T.W.;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF177668; AAF00915.1; -.
HSSP; P23906, 21RF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0267; INTERNREGECT.
PROSITE; PS00601; IRF; 1.
NOM_TER 1 1 1
NOM_TER 330 330
SEQUENCE 330 AA; 37355 MW; EB02EC8B751CBD7D CRC64;
                                                                                                                                                                                            CHAIN 28 293 POTENTIAL.
SEQUENCE 293 AA; 31128 MW; DB1B21728F657F2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                            POTENTIAL.
HYDROLASES).

EMBL; Y16415; CAA76203.1; -.

EMSP; P23472; 2HVM.

Mendel; 28297; Lupal;Chib1;28297.

InterPro; IPR001579; -.

Pfam; PF00192; chitinase_2; 1.

PROSITE; PS01095; CHITINASE_18; 1.

Glycosidase; Hydrolase; Signal.

SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2001 (TrEMBLrel. 16, Last ann
C40HS.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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142 GIDFDIEAGGAQHYDELARAL 162
                                                                                                                                                                                                                                                                                                                                                                  1 GETFOVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250 QVKFPGPEHITNEKQKL 266
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Best Local Similarity 41.2
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IRF6 (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0902L7;
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DR DR DR DR SO FT TW
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Chol Y., Spencer T.E., Bazer F.W.;
Choling and Analysis of Covine IRF-6.";
L Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL; AF228446; AAF34782.1; -.
R Interpro; IPR001346; -.
R Pfan; PF00605; IRF; 1.
R PRINTS; PR00255; INTFRNREGFCT.
R PROSURE; PS00601; IRF; 1.
R PROSURE; PS00601; IRF; 1.
SEQUENCE 467 AA; 52970 MW; 21E04F749844D88F CRC64;
                                                                                                                                                                                                                                                    Query Match
41.1%; Score 44; DB 5; Length 374;
Best Local Similarity 42.1%; Pred. No. 41;
Matches 8; Conservative 2; Mismatches 9; Indels
                                                                                                     "Genome sequence of the nematode C.elegans: A platform for investigating biology."; sclence 282:2012-2018(1989). EMBL; Z81482; ca803954.2; -. SEQUENCE 374 AA, 42198 MW; 67D202886D6A7824 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 467;
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                             MEDLINE-99069613; PubMed-9851916;
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                                                                                                                                                                                                                                                                                                                                        1 GETFQVEVPGSQHIDSQKK 19
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Search completed: July 16, 2001, 16:43:39
Job time: 473 sec
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Schulte U., Adyn V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                      Gaps
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                        STRAIN-BALB/C; TISNEY, GENOMIC DNA 129/J STRAIN (DR. J. ROSSANT); Grossman A., Mittrucker H.W., Antonio L., Mak T.W.; Submitted (QCT-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                          Score 44; DB 11; Length 467;
Pred. No. 53;
6; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41.1%; Score 44; DB 3; Length 864;
42.1%; Pred. No. 1e+02;
tive 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               German Neurospora genome project;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; A1355930; CAB91375.1;
Interpro; IRNO0542;
Pfam; PF00755; Carn_acyltransf; 1.
PROSITE; PS00440; ACYLTRANSF_C_2; UNKNOWN_1.
                                                                                                                                                                                                            68CCAA90680FEDC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               864 AA; 94444 MW; E6FE698AE507AF6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PROBABLE CARNITINE ACETYL TRANSFERASE FACC.
                                                                                                                                                                                                                                                                                                                                                                        864 AA.
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                                                                                                                           MCD; MGI:1859211; Irf6.
InterPro: IPR001346; -.
Pfam; PF00605; IRF; 1.
PRINTS; PR00257; INTERNEGECT.
PRODOM; PD002355; -; 1.
PROSITE; PS00601; IRF; 1.
                                                                                                                                                                                                SMART; SM00348; IRF; 1.
SEQUENCE 467 AA; 53106 MW;
                                                                                                                                                                                                                                             41.18;
                                                                                                     EMBL; U73029; AAB36714.1; -. HSSP; P23906; 2IRF.
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Best Local Similarity 41.2
Matches 7; Conservative
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Best Local Similarity 42.1
Matches 8; Conservative
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                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurospora crassa.
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                       NCBI_TaxID=10090;
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Q9SKB2
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MEDILINE-20083487; PubMed-10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Feldblyum T.V.,
Eujil C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., Vanaken S.E., Umayam L.J., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome II of Arabidopsis thaliana.";
Nature 402:761-768(1999).
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                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00370; LRR; 1.
ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
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7;
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50.0%; Pred. No. 89;
Live 3; Mismatches
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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InterPro; IPR003592; -.
Pfam; PF00069; pkinase; 1.
Pfam; PF00560; LRR; 4.
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Best Local Similarity 50.0%
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From: Sent:

Ford, Vanessa Wednesday, October 23, 2002 12:15 PM STIC-Biotech/ChemLib Sequence search 09/786648

To: Subject:

Please search SEQ ID Nos: 2, 3, 4, and 5.

Please include inteference searches.

Vanessa L. Ford

**Biotechnology Patent Examiner** 

Office: CM1 8B13 Mailbox: CM1 8E12 Phone: 703.308.4735 CRFF

Point of Contact: Susan Hanley Technical Info. Specialist CM1 6B05 Tel: 305-4053 This Page Blank (uspto)